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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the brain and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S.provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entirety.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_BRAIN.txt, created
25 24 January 2001, having 25,840,972 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

brain and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.
25 There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the brain and nervous system particularly those diseases with polygenic etiology.

30 Summary of the Invention

 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional
35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single
15 exon nucleic acid probes for measuring gene expression in a sample derived from human brain, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,434 or a complimentary sequence, or a
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is
20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,822 - 25,434, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,821.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

12,822 - 25,434 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 - 37,811 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high
10 stringency to a nucleic acid expressed in the human brain.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
15 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
20 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
25 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent
35 labels include dyes such as cyanine dyes, preferably Cy3

and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third
5 or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

10 In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the
15 invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample
20 derived from human brain, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of
25 human brain; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic
30 genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

35 wherein said detectably labeled nucleic acids are

derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
5 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
10 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
15 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
20 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,434 wherein said sequence encodes a peptide.

25 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,822 - 25,434, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
30 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,821.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
35 ID NOS.: 25,435 - 37,811.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 - 37,811, or fragment thereof.

5 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
10 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

15

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
20 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
25 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary
35 planar substrate, as is described, *inter alia*, in Brenner

et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

5 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick
10 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

 As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid
15 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the
20 requirement that the probe hybridize to mRNA.

 As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence
25 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

 As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing
30 the predicted exon.

 As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
35 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a
5 portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a
10 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF
15 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another
20 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit
25 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display
30 of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual
35 object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original

sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence
5 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A
10 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

15 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can
20 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part
25 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
30 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the
35 National Center for Biotechnology Information (NCBI).

Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic
5 sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by
10 the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into
15 mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into
20 process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will
25 be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental
30 confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the
35 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in

subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is

possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional

preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable
5 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to,
10 or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and
15 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual
20 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,
25 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known
30 restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be
35 removed. Removal can usefully be done by masking the

undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired
5 sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower
10 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest
15 contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*,
20 addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as
25 conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting
30 such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating
35 transcription, regulating message transport after

transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability
5 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function
10 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as
15 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for
20 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)
25 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene
30 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
35 and DICTION yielded the least putative coding region, with

0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, 5 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such 10 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored 15 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further 20 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 25 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three 30 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used 35 approach to exon calling is gene prediction, the process

can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison
5 can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the
10 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
15 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to
20 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon
25 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene
30 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
35 secondary structure, and the like can be used to identify

and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at

amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

5 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic
10 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased
15 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves
20 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later
25 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least
30 about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
35 amplification will come from the eukaryotic species from

which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, 5 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, 10 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

15 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination 20 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or 25 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

30 As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can 35 readily be used. As further described in Example 1, 16 or

32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
5 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
10 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
15 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
20 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
25 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
30 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
35 throughput and compatibility with existing readers. For

example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
5 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
10 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
20 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
25 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al.,
or from the *de novo* construction of "problem specific"
30 libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST, microarrays".

Such EST microarrays by definition can measure
35 expression only of those genes found in EST libraries,

shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective
5 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be
10 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the
15 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA
20 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays..

25 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present
30 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
35 transcription and cloning of unknown message in EST

approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, 5 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric 10 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome- 15 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present 20 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the 25 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically 30 include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector 35 sequence, having been amplified directly or indirectly from

genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly
5 lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through
10 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-
15 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker
20 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include
25 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to
30 the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
35 such sequences, and if so constructed, presents an even

smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
5 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
10 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
15 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
20 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often
25 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
30 probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

35 In contrast, by virtue of their origin from

algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 5 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single 10 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression 15 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 20 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon 30 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and 35 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic
5 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to
10 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present
20 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved
25 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention
30 typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their
35 complementary target sequence, and thus causes large

percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower
5 percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual
10 probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the
15 present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear
20 genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the
25 ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present
30 invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence
35 drawn from eukaryotes in which at least about 10, 20 or 50%

of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which
5 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

10 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization
15 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the
20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can
25 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see
30 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
35 nucleotides labeled with a first label, typically a

fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
5 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

10 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
15 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
20 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
25 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
30 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
35 can be used, greater efficiency is obtained using higher

density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
5 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
10 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
15 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

20 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

25 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
30 set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing
35 information, and that can additionally contain annotation

information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate
5 that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

10 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a
15 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental
20 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be
25 compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide
30 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local
35 alignment search tool"). The results of such query -

including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence — can then be passed directly to process 500, or used to
5 inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data
10 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or
15 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or
20 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence
25 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic
30 works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
35 the number of nucleotides typically represented in an

annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
5 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

10 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
15 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically — for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
20 pointer over rectangle 89 — or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
25 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
30 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity
35 or identity to an input query sequence. When visual

display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection
5 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional
10 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

15 Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method
20 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

25 Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c
30 represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.
35 For example, rectangles 83a can represent the results from

GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as

many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
5 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be
10 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical
15 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of
20 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of
25 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to
30 depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to
35 indicate expression intensity. As discussed *infra*, such

relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is

protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

10 It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,821 of these ORFs in brain.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in brain is currently available for use in measuring the level of its ORF's expression in brain.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

For example, over the past few decades Alzheimer's disease (AD), once considered a rare disorder,

has become recognized as a major public health problem; over 4,000,000 people in the United States are now estimated to suffer with various stages of this progressive, degenerative brain disorder.

5 Although there is no agreement on the exact incidence or prevalence of Alzheimer's disease, in part due to varying diagnostic criteria and difficulties of differential diagnosis among dementias, the studies are consistent in pointing to an exponential rise in prevalence
10 of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2
15 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

 Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest of tasks. Anatomic
20 changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and
25 internal neurofibrillary tangles.

 Alzheimer's disease has been suspected to have a multifactorial genetic etiological component for almost half a century. Sjogren et al., Acta Psychiat. Neurol. Scand. 82(suppl.): 1-152 (1952).

30 At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with the APOE4 allele on chromosome 19; AD3 is caused by mutation in a chromosome 14 gene encoding
35 a 7-transmembrane domain protein, presenilin-1 (PSEN1), and

AD4 is caused by mutation in a gene on chromosome 1 that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2).

There is strong evidence, however, for additional, as yet uncharacterized, AD loci on other chromosomes.

For example, Daw et al., Am. J. Hum. Genet. 66: 196-204 (2000), estimated the number of additional quantitative trait loci (QTLs) and their contribution to the variance in age at onset of AD, and reported that 4 loci make a contribution to the variance in age at onset of late-onset AD similar to or greater in magnitude than that made by apoE, with one locus making a contribution several times greater than that of apoE. These results suggest that several genes not yet localized may play a larger role than does apoE in late-onset AD.

In accord, three groups recently announced the possible existence of an AD susceptibility gene on chromosome 10. Bertram et al., Science 290(5500):2302-2303 (2000); Ertekin-Taner et al., Science 290(5500):2303-2304 (2000); and Myers et al., Science 290(5500):2304-2305 (2000).

As another example, multiple sclerosis (MS) affects about 350,000 Americans, with approximately 200 new cases diagnosed each week, with an estimated annual monetary cost in the U.S. alone of \$2.5 billion.

Clinically, MS is an unpredictable disorder, with symptoms, presentation and course falling broadly into one of several clinical patterns. In relapsing-remitting (RR) MS, the disease first manifests as a series of attacks followed by complete or partial remissions, with symptoms returning later after a period of stability. In primary-progressive (PP) MS, there is a gradual clinical decline with no distinct remissions, although there may be

temporary plateaus or minor relief from symptoms.

Secondary-progressive (SP) MS begins with a relapsing-remitting course followed by a later primary-progressive course. Rarely, patients may have a progressive-relapsing (PR) course in which the disease takes a progressive path punctuated by acute attacks. PP, SP, and PR MS are sometimes lumped together and called chronic progressive MS. The waxing and waning course characteristic of RR, SP and PR MS makes differential diagnosis difficult.

10 Anatomically, MS attacks are associated with focal inflammation in areas of the white matter of the central nervous system (CNS), accompanied or followed by demyelination in these areas, termed plaques. Destruction of the myelin sheath slows or blocks neurological
15 transmission, leading to diminished or lost function. Clinical manifestations depend upon the location of the plaques and severity of demyelination, and range from fatigue, the most common symptom of MS, to visual impairment, due to inflammation of the optic nerve, termed
20 optic neuritis, to numbness and paresthesias, to focal muscular weakness, ataxia, and bladder incontinence.

Increasing evidence suggests that genotype contributes to susceptibility to MS.

As early as 1965, McAlpine, in Multiple
25 Sclerosis: A Reappraisal (McAlpine, ed.), Williams and Wilkins Co. pp. 61-74 (1965), concluded that the risk to a first-degree relative of a patient with multiple sclerosis is at least 15 times that for a member of the general population, but could discern no definite genetic pattern
30 of inheritance.

Subsequently, many studies associated MS with HLA (MHC) haplotype. Haines et al., Hum. Molec. Genet. 7:1229-1234 (1998), studying a data set of 98 multiplex MS families, confirmed earlier reports that genetic linkage to
35 the MHC can be explained by association with the HLA-DR2

allele, but suggested that MHC association explains only between 17% and 62% of the genetic etiology of MS.

From a review of genomic screens, Dyment et al., Hum. Molec. Genet. 6: 1693-1698 (1997), concluded that a number of genes with interacting effects are likely and that no single region has a major influence on familial risk. Chataway et al., Brain 121: 1869-1887 (1998), reporting a follow-up on U.K. studies using a systematic genome screen to determine the genetic basis of MS, stated that a gene of major effect had been excluded from 95% of the genome and one with a moderate role from 65%, results thus suggesting that multiple sclerosis depends on independent or epistatic effects of several genes, each with small individual effects, rather than a very few genes of major biologic importance.

As a yet further example, schizophrenia has long been recognized to have complex, likely polygenic, genetic contributions.

Schizophrenia is a common psychiatric disorder, occurring in 1 to 1.5 percent of the population worldwide, and is characterized by variable constellations of symptoms drawn from a universe of behavioral abnormalities. Although there are accepted alternative diagnostic criteria, primary criteria for diagnosis require two or more of the following, each present for a significant portion of time during a 1-month period (or less if successfully treated): (1) delusions; (2) hallucinations; (3) disorganized speech (e.g., frequent derailment or incoherence); (4) grossly disorganized or catatonic behavior; (5) negative symptoms, i.e., affective flattening, alogia, or avolition. (Diagnostic and Statistic Manual of Mental Disorders DSM-IV-TR, American Psychiatric Association (2000)). Only one such symptom is required if delusions are bizarre or hallucinations consist of a voice keeping up a running commentary on the

person's behavior or thoughts, or consist of two or more voices conversing with each other.

Three-quarters of persons with schizophrenia develop the disease between 16 and 25 years of age: onset is uncommon after age 30, rare after age 40. In the 16 to 25 year old age group, schizophrenia affects more men than women; in the 25-30 year old group, the incidence is higher in women than in men. Studies have shown that some persons with schizophrenia recover completely, and many others improve to the point where they can live independently, often with the maintenance of drug therapy. However, approximately 15 percent of people with schizophrenia respond only moderately to medication and require extensive support throughout their lives, while another 15 percent simply do not respond to existing treatment.

Schizophrenia has long been known to have a significant genetic component. Studies have consistently demonstrated that the risk to relatives of a proband with schizophrenia is higher than the risk to relatives of controls. Moldin, in Genetics and Mental Disorders: Report of the NIMH Genetics Workgroup (NIH publication 98-4268, (1998), reviewed family and twin studies published between 1920 and 1987 and found the recurrence risk ratios to be 48 for monozygotic twins, 11 for first-degree relatives, 4.25 for second-degree relatives, and 2 for third-degree relatives. He also found that concordance rates for monozygotic twins averaged 46%, even when reared in different families, whereas the concordance rates for dizygotic twins averaged only 14%. The prevalence of schizophrenia is known to be higher in biologic than in adoptive relatives of schizophrenic adoptees.

The mode of inheritance is unclear, however. Susceptibility has been mapped to many loci, including chromosomes 1q21-q22, 5, 6p23, 8p22-p21, 11q, 13q14-q21, 13q32, 15q15, 15q14, 18p, and 22q11. Chromosome

19 has also been implicated in schizophrenia, at 2
different sites, as have sites on the X chromosome. Wei et
al., Nature Genet. 25:376-377 (2000) report more
specifically that the NOTCH4 locus is associated with
5 susceptibility to schizophrenia.

In general, however, it is believed that
development of schizophrenia involves multiple loci.

For example, Williams et al., Hum. Molec. Genet.
8:1729-1739 (1999) undertook a systematic search for
10 linkage in 196 affected sib pairs (ASPs) with
schizophrenia. Using 229 microsatellite markers at an
average intermarker distance of 17.26 cM, followed in a
second stage by a further 54 markers allowing the regions
identified in stage 1 to be typed at an average spacing of
15 5.15 cM, Williams et al. considered results on chromosomes
4p, 18q, and Xcen as suggestive; however, given the scores,
Williams et al. interpreted their results as suggesting
that common genes of major effect (susceptibility ratio
more than 3) are unlikely to exist for schizophrenia.

20 Similarly, Shaw et al., Am. J. Med. Genet.
81(5):364-76 (1998), in a genome-wide search for
schizophrenia susceptibility genes, found that twelve
chromosomes (1, 2, 4, 5, 8, 10, 11, 12, 13, 14, 16, and
22) had at least one region with a nominal P value <0.05,
25 that two of these chromosomes had a nominal P value <0.01
(chromosomes 13 and 16), and that five chromosomes (1, 2,
4, 11, and 13) had at least one marker with a lod score
>2.0, suggesting the existence of multiple loci that
contribute to schizophrenia susceptibility.

30 As yet another example, multiple genes are
thought to predispose to epilepsy.

Epilepsy is characterized by recurrent,
paroxysmal disorders of cerebral function (seizures); that
is, by sudden, brief attacks of altered consciousness,
35 motor activity, sensory phenomena, or inappropriate

behavior. The risk of developing epilepsy is 1% in the period from birth to age 20, and 3% at age 75.

Epilepsy is caused by excessive discharge of cerebral neurons. Clinical manifestations depend on the type and location of discharge. In partial seizures, for example, the excess neuronal discharge is contained within one region of the cerebral cortex. Simple partial seizures consist of motor, sensory, or psychomotor phenomena without loss of consciousness; the specific phenomenon reflects the affected area of the brain. In generalized seizures, the discharge bilaterally and diffusely involves the entire cortex. Sometimes a focal lesion of one part of a hemisphere activates the entire cerebrum bilaterally so rapidly that it produces a generalized tonic-clonic seizure before a focal sign appears.

Epilepsy is a family of disorders. Those that are idiopathic are believed to have multiple genetic contributions. For example, idiopathic generalized epilepsy (IGE) is characterized by recurring generalized seizures in the absence of detectable brain lesions and/or metabolic abnormalities. Twin and family studies suggest that genetic factors play a key part in its etiology. Although a mutation in the CACNB4 gene can cause the disorder, linkage to 8q24, Zara et al., Hum. Molec. Genet. 4: 1201-1207(1995), 3q26 and 14q23, Sander et al., Hum. Molec. Genet. 9:1465-1472 (2000), and 2q36 has been also demonstrated, with a multilocus model appearing to fit best the observed familial patterns.

Polygenic contributions to the etiology of various neurologic cancers have similarly been described.

For example, gliomas account for 45% of intracranial tumors, and multiple loci have been implicated in its development, with losses of chromosome 17p, increase in copy number of chromosome 7, structural abnormalities of

chromosomes 9p and 19q, and genes on chromosome 10 among the suspects.

Other significant diseases of brain and nervous tissue are also believed to have a genetic, typically
5 polygenic, etiologic component. These diseases include, for example, Parkinson's disease, dementia with Lewy bodies, frontotemporal dementia, corticobasal ganglionic degeneration, progressive supranuclear palsy, prion diseases (Creutzfeld-Jakob, Gerstmann-Straussler-Shenker,
10 familial fatal insomnia), Tourette's Syndrome, corticobasal degeneration, multiple system atrophy, striatonigral degeneration, Shy-Drager syndrome, olivopontocerebellar atrophy, spinocerebellar ataxia, Friedreich ataxia, ataxia-telangiectasia, amyotrophic lateral sclerosis, bulbosplinal
15 atrophy (Kennedy's syndrome), spinal muscular atrophy, neuronal storage diseases (sphingolipid, mucopolysaccharide, mucolipid), leukodystrophy, Krabbe disease, metachromic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Canavan disease,
20 mitochondrial encephalomyopathy, Leigh disease, neurofibromatosis (Type I and Type II), tuberous sclerosis, paraneoplastic syndrome, subacute cerebellar degeneration, subacute sensory neuropathy, opsoclonus/myoclonus, retinal degeneration, stiff-man syndrome and Von Hippel-Lindau
25 disease.

Many neurologic cancers other than gliomas have also been shown or suspected to have genetic bases or contributions. Among these cancers are astrocytoma, fibrillary astrocytoma, pilocytic astrocytoma,
30 pleomorphic xanthoastrocytoma, oligodendroglioma, ependymoma, gangliocytoma, ganglioglioma, medulloblastoma, primary brain germ cell tumor, pineocytoma, pineoblastoma, and meningioma.

Other disorders of brain and central nervous
35 system that likely have genetic components include the

various forms of neural deafness, catatonia, depression, bipolar (manic-depressive) disorder, Wilson's Disease, Pick disease, neuromyelitis optica (Devic disease), central pontine myelinolysis, Marchiafava-Bignami disease, 5 Guillain-Barre syndrome, sleep disorders (insomnia, myoclonus, narcolepsy, cataplexy, sleep apnea), amnesia, aphasias (including Broca's aphasia and Wernicke's aphasia), cortical blindness, visual agnosia, auditory agnosia, and Kluver-Bucy syndrome.

10 The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human brain, particularly those diseases with polygenic etiology. With each of the single 15 exon probes described herein shown to be expressed at detectable levels in human brain, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 25 to be characteristic of a given neurologic disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 30 patient's brain (or other CNS tissues, including cultured tissues) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating 35 gene expression profiles, without regard to the function of

the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be
5 used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of neurologic disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's
10 genome of exons known to be expressed in human brain. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at
15 sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the
20 probes of the present invention, for which expression in the brain has been demonstrated are useful for both measurement in the brain and for survey of expression in other tissues.

Significant among such advantages is the presence
25 of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which
30 the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of
35 only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15 Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);
35 Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway
35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena *et al.*

The invention particularly provides genome-derived single-exon probes known to be expressed in brain.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are

described, for example, in U.S. Patent Nos. 5,142,047;
5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
form and quantity suitable for amplification, where the
5 amplified product is thereafter to be used in the
hybridization reactions that probe gene expression.
Typically, such probes are provided in a form and quantity
suitable for amplification by PCR or by other well known
amplification technique. One such technique additional to
10 PCR is rolling circle amplification, as is described, *inter
alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and
international patent publications WO 97/19193 and
WO 00/15779. As is well understood, where the probes are
to be provided in a form suitable for amplification, the
15 range of nucleic acid analogues and/or internucleotide
linkages will be constrained by the requirements and nature
of the amplification enzyme.

Where the probe is to be provided in form
suitable for amplification, the quantity need not be
20 sufficient for direct hybridization for gene expression
analysis, and need be sufficient only to function as an
amplification template, typically at least about 1, 10 or
100 pg or more.

Each discrete amplifiable probe can also be
25 packaged with amplification primers, either in a single
composition that comprises probe template and primers, or
in a kit that comprises such primers separately packaged
therefrom. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
30 common sequence added thereto, and the ORF-specific 3'
primers used for genomic amplification can have a second,
different, common sequence added thereto, thus permitting,
in this embodiment, the use of a single set of 5' and 3'
primers to amplify any one of the probes. The probe
35 composition and/or kit can also include buffers, enzyme,

etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,822 - 25,434, respectively, for probe SEQ ID NOS. 1 - 12,821. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or

microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,822 - 25,434 individually by routine experimentation using standard high stringency conditions.

5 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a
10 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization
15 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room
20 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single
25 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more
30 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more
35 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member

of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human brain.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in

Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term
5 "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human brain.
10 In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,821.

When used for gene expression analysis, the
15 genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray
20 surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a
25 fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means
30 can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon
35 microarray, each of the nucleic acids having SEQ ID NOS.: 1

- 12,821 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,822 - 25,434, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,821 can be used, or that portion thereof in SEQ ID NOS. 12,822 -
5 25,434 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as
10 protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New
15 England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide
20 Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles
25 of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,822 - 25,434. Such amino
30 acid sequences are set out in SEQ ID NOS: 25,435 - 37,811. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a
35 further aspect of the invention to provide peptides that

have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

10

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and

DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding
5 region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a
10 single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

15 PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes
20 were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore,
25 amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3
30 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit
35 subsequent reamplification of the amplicon using a single

set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant
5 further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

10 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of
15 agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest
20 directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range
25 of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR
amplification product contained predicted coding region,
30 with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process
35 was adjusted to amplify 1000, 1500 or 2000 bp fragments

from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

- 5 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and
10 standard protocols.

 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some
15 submitted sequence data.

 Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression
20 ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not
25 shown).

 The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII
30 Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

35 Each of the probe sequences was BLASTed against

the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal

45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 25 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 30 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT,

100 μ M dATP, 100 μ M dGTP, 100 μ M dTTP, 50 μ M dCTP, 50 μ M
Cy3-dCTP or Cy5-dCTP 50 μ M, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
5 1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
10 for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
Speedvac, resuspended in 30 μ l hybridization solution
containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2
 μ g/ μ l human cot1 DNA, and 0.5 % SDS.

15 Hybridizations were carried out under a
coverslip, with the array placed in a humid oven at 42°C
overnight. Before scanning, slides were washed in 1X SSC,
0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%
SDS, at 55°C for 20 minutes. Slides were briefly dipped in
20 water and dried thoroughly under a gentle stream of
nitrogen.

Slides were scanned using a Molecular Dynamics
Gen3 scanner, as described. Schena (ed.), Microarray
Biochip: Tools and Technology, Eaton Publishing
25 Company/BioTechniques Books Division (2000) (ISBN:
1881299376).

Although the use of pooled cDNA as a reference
permitted the survey of a large number of tissues, it
attenuates the measurement of relative gene expression,
30 since every highly expressed gene in the tissue/cell type-
specific fluorescence channel will be present to a level of
at least 10% in the control channel. Because of this fact,
both signal and expression ratios (the latter hereinafter,
"expression" or "relative expression") for each probe were
35 normalized using the average ratio or average signal,

respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the

matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST

database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

30

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)

and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be

biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system

AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen

AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
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Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to

tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2
were similar to actin (AL035701-2; AL034402-1), and 6 were
found to be homologous to glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
5 AC006064-K; AC035604-3; AC006064-L). These genes are often
used as controls or housekeeping genes in microarray
experiments of all types.

Other interesting genes highly expressed in brain
were a ferritin heavy chain protein, which is reported in
10 the literature to be found in brain and liver (Joshi et
al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result
duplicated with the array. Other highly expressed chip
sequences included a translation elongation factor 1 α
(AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
15 chromosome RNA-binding motif (Chai et al., *Genomics*
49(2):283-89 (1998)) (AC007320-3). A low homology analog
(AP00123-1/2) to a gene, DSCR1, thought to be involved in
trisomy 21 (Down's syndrome), showed high expression in
both brain and heart, in agreement with the literature
20 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we
selected the BAC AC006064 to be included on the array.
This BAC was known to contain the GAPDH gene, and thus
could be used as a control for the ORF selection process.
25 The gene finding and exon selection algorithms resulted in
choosing 25 exons from BAC AC006064 for spotting onto the
array, of which four were drawn from the GAPDH gene. Table
3 shows the comparison of the average expression ratio for
the 4 exons from BAC006064 compared with the average
30 expression ratio for 5 different dilutions of a
commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe

sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure,

it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they
5 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
10 turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

15 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2,
20 *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in brain tissue.

These unique exons are within longer probe
25 sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-
30 incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented
35 fragments of each of the 12,821 single exon probes, each

fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,821 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,821. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID NOS.: 12,822 - 25,434, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the

observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified
5 control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

10 This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.
15 Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human brain tissue.

20 The sequence of each of the exon probes identified by SEQ ID NOS.: 12,822 - 25,434 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because
25 the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the
30 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were
35 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences
5 (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity
10 to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E
15 Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not
20 have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons,
25 without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,821) and probe exon (SEQ ID NOs.: 12,822 - 25,434,
30 respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about
35 the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Brain

15

Table 4 (536 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human brain.

20

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human brain comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,822 - 25,434.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human brain.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,822 - 25,434 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOs.: 25,435 - 37,811, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

16. A single exon nucleic acid probe as claimed in any one.
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human brain, comprising:

5 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human brain; and then
 measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

 algorithmically predicting at least one exon from
15 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
from mRNA from the brain of said eukaryote, said probe is a
20 single exon probe having a fragment identical in sequence
to, or complementary in sequence to, said predicted exon,
said probe is included within a microarray according to
claim 12, and said fragment is selectively hybridizable at
high stringency.

25

24. A method of assigning exons to a single gene, comprising:

 identifying a plurality of exons from genomic
 sequence according to the method of claim 23; and
30 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
 probe with said exon,
35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 25,434 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 25,434.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID NOS: 25,435 - 37,811.

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
437	13223	25868	6.47				
869	13638	26308	15.92				
1022	13782		2.15				
1279	14028	26698	10.88				
1488	14235	26921	1.22				
1488	14235	26922	1.22				
1809	14355	27044	3.19				
1833	14379	27068	6.1				
1718	14481	27160	3.31				
1743	14485	27184	1.44				
1750	14492	27192	6.78				
1884	14621	27331	1.44				
1971	14707	27425	2.14				
2162	14892	27627	2.7				
2277	15003	27743	2.91				
2578	15292	28028	1				
2578	15292	28028	1				
3181	15944	28595	2.83				
3442	16198	28848	1.42				
3505	16261	28915	12.04				
3549	16304		1				
3549	16402	29042	1.67				
3928	16678		1.03				
4173	16913	29543	1.52				
4230	16971	29595	6.4				
4248	16989	29613	0.97				
4248	16989	29614	0.97				
4303	17042		1.07				
4361	17069	29734	0.76				
4784	17516	30138	0.99				
4983	17706	30310	6.38				
4995	17718	30323	1.3				
5176	17985	30500	1.57				
5176	17985	30501	1.57				

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5336	18139		4.3				
5510	18308		6.14				
5593	18139		3.97				
5648	18443	31356	0.6				
5654	18449	31362	3.28				
5932	25082	31673	1.62				
5958	18740	31698	1.76				
6322	18092		1.27				
6454	19222	32220	1.1				
6454	19222	32221	1.1				
7025	19717	32774	1				
7025	19717	32775	1				
7311	19994	33071	1.76				
7311	19994	33072	1.76				
7712	20376		0.61				
7960	20655	33780	1.4				
8384	21077	34214	1.49				
8759	21451	34598	0.59				
8759	21451	34599	0.59				
9434	22112	35287	2.67				
9666	22318	35515	0.77				
9782	22433	35638	1.24				
9922	22570	35767	0.94				
10328	22875	36184	0.62				
10328	22975	36195	0.62				
10582	23277		2.53				
10749	25131	36679	1.34				
10952	23629		2.2				
11030	23701	36968	1.84				
11332	24023	37328	2.02				
11485	24098		2.47				
12313	24735		1.52				
12609	24916	31006	2.36				
5861	18743	31703	17.79	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7905	20600	33730	1.74	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9843	22295	35489	0.44	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9843	22295	35490	0.44	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
6901	19839	32694	0.73	9.6E+00	AF066630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
6901	19839	32695	0.73	9.6E+00	AF066630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10321	22968	36187	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
10321	22968	36188	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2671	15381	28119	1	9.4E+00	L11433.1	NT	Dangue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2671	15381	28120	1	9.4E+00	L11433.1	NT	Dangue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2624	15690	28334	2.87	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
7997	20692	33820	0.91	9.3E+00	AF130980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8901	21592	34733	3.06	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5214	18022	30645	2.46	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5214	18022	30646	2.46	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
8930	21997		0.83	9.0E+00	P09241	SWISSPROT	RHODOPSIN
5945	18727	31695	5.55	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6287	19060	32041	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6287	19060	32042	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
430	13216	25861	2.3	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9355	20426	33545	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11122	23791		2	8.0E+00	P41820	SWISSPROT	BREFELIN A RESISTANCE PROTEIN
8051	20745		0.89	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7246	19931		1.9	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8259	20953	34090	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8259	20953	34091	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5711	18504	31426	2.66	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285508 5'
8651	21343	34487	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8651	21343	34488	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2977	15743	28390	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2977	15743	28391	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6931	19867	32713	0.71	7.2E+00	BE179090.1	EST_HUMAN	RC00-110613-200300-031-a07 HT0613 Homo sapiens cDNA
7049	19740	32800	1.28	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7049	19740	32801	1.28	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9498	22151		8.63	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11359	24047	37350	3.28	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
9882	22532	35729	3.37	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11215	23878	37165	1.51	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8181	20875	34011	1.92	6.8E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10249	22897	36107	1.38	6.8E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10267	22915	36125	0.47	6.9E+00	P34228	SWISSPROT	SKT5 PROTEIN
7808	20503	33623	1.53	6.8E+00	W03412.1	EST_HUMAN	z07c11.1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:281860 5'
7808	20503	33624	1.53	6.8E+00	W03412.1	EST_HUMAN	z07c11.1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:281860 5'
							OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) (CONTAINS:
							OUTER CAPSID PROTEINS VP5 AND VP8]
9031	21721		1.28	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8]
10109	22757	35969	3.24	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5202	18010		0.72	6.6E+00	Q88028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6450	19218	32216	0.61	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283427 5'
9974	22622	35827	2.36	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9974	22622	35828	2.36	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11073	23743		1.97	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9078	21768	34931	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10203	22851	36067	0.49	6.5E+00	BE866001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'
9842	22294	35488	1.55	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
10460	23106	36337	0.5	6.2E+00	6754621	NT	Mus musculus memosidase 2, alpha B1 (Mem2b1), mRNA
6838	19871	32717	1.46	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
9716	22367	35565	0.46	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt position (877)
10411	23057	36274	0.57	6.0E+00	AE001882.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10411	23057	36275	0.67	6.0E+00	AE001882.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
							Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
6428	19186	32163	7.32	5.9E+00	AF155142.1	NT	complete cds
3514	16270		0.99	5.8E+00	7681557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7061	19752	32816	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7091	19752	32817	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7468	20142		1.13	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11456	23223	36458	2.59	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
6157	18934	31901	0.89	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10678	23369		1.28	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11454	23221	36455	3.09	5.5E+00	P11980	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
6830	19492	32514	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
6830	19492	32515	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7769	20465		1.54	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8698	21390	34534	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8698	21390	34535	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8636	22584	35784	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
8636	22584	35785	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4734	17486	30102	1.32	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
7978	20673		3.23	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8862	21573		0.49	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11628	24225	37548	3.2	5.3E+00	Q27805	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
6377	18177		0.91	5.2E+00	BE184840.1	SWISSPROT	QV4-HT0691-270400-186-609 HT0691 Homo sapiens cDNA
10271	22819		0.85	5.2E+00	AF249070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11150	23817		2	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
8861	21552	34698	0.9	5.1E+00	O16005	SWISSPROT	RHODOPSIN
9725	22376	35577	1.19	5.1E+00	P09182	SWISSPROT	GOLGIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6193	18969	31944	0.72	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10094	22742		0.69	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10330	22877	99197	3.07	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11260	23622	37214	8.95	5.0E+00	Z33860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10132	22780		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, R6Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds
4039	16784		10.88	4.8E+00	AF185255.1	NT	Euroca australis histone H3 (H3) gene, partial cds
8054	20748	33879	0.47	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8439	21131		5.28	4.8E+00	AW750067.1	EST_HUMAN	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
283	13090	25731	1.86	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
284	13080	25731	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3268	16030	28879	2.38	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9085	21783	34948	1.18	4.6E+00	BE948437.1	EST_HUMAN	7e88g10.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3282088 3' similar to TR:O75140 O75140 KJAA0045 PROTEIN; contains element PTR5 repetitive element;
9085	21783	34948	1.18	4.6E+00	BE848437.1	EST_HUMAN	7e88g10.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3282088 3' similar to TR:O75140 O75140 KJAA0045 PROTEIN; contains element PTR5 repetitive element;
10287	22935		0.81	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11054	23724		2.31	4.6E+00	D63898.1	NT	Synechocystis sp. PCC6803 complete genome, 1827, 2287260-2382728
11605	24204	37628	2.59	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11762	24353	37895	1.78	4.5E+00	BF68841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3035	15801	28447	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3035	15801	28448	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6109	18896		1.68	4.4E+00	X13414.1	NT	Murine I gene for MHC class II (a) associated invariant chain
6027	18807		0.68	4.3E+00	AF059678.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7338	20019	33097	2.03	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
7515	20186	33280	0.65	4.3E+00	AE001222.1	NT	Treporema pallidum section 38 of 87 of the complete genome
10769	23453	36696	7.64	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5430	18229		3.44	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5507	18305	31206	0.87	4.2E+00	P51826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6674	18591	32627	2.62	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6674	18591	32628	2.62	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8859	21550	34697	4.68	4.2E+00	AB00013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
9818	22469	35672	1.08	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-18) (DOCT1)
10049	22697		0.46	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8
5846	25079	31559	0.56	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
5846	25079	31570	0.58	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7012	19704	32760	0.84	4.1E+00	BE253688.1	EST_HUMAN	60110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7111	19789	32863	0.65	4.1E+00	BF247838.1	EST_HUMAN	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:40669758 5'
7559	20228	33332	8.73	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7681	20345		0.62	4.1E+00	AB041523.1	NT	Painopecten yessoensis mRNA for calcineurin A, complete cds
7683	20347	33459	4.32	4.1E+00	P28984	SWISSPROT	GENE 68 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7683	20347	33460	4.32	4.1E+00	P28904	SWISSPROT	GENE 68 PROTEIN
7817	20512	33638	2.53	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9440	22118	35295	0.57	4.1E+00	P11263	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9571	22224	35409	2.48	4.1E+00	BF692425.1	EST_HUMAN	602247838F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10205	22853		0.48	4.1E+00	P48414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
10800	23483		3.06	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVL1
10892	23572		11.69	4.1E+00	BE885980.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3533	16289		0.95	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5372	19500	32524	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5372	19500	32525	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32524	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32525	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7089	19778	32843	1.44	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8772	21464	34611	0.45	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
9843	22494	35695	0.44	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10065	22713	35931	0.63	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 69 of the complete genome
11453	23220	36454	1.53	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11537	24137	37444	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS2C, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11537	24137	37445	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3494	16250	28904	4.61	3.9E+00	X84518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4287	17026		8.24	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 98 (MSVSP98) gene, promoter region
5572	18369	31279	2.91	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5572	18369	31280	2.91	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6591	19354	32567	0.55	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
6774	19518	32546	4.62	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIB-RPSF INTERGENIC REGION

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7262	18948	33022	4.3	3.9E+00	M23907.1	NT	Human MHG class II lymphocyte antigen (DPW4-beta-1) gene, exon 2
8216	20910	34046	1.86	3.8E+00	X65865.1	NT	X laevis mRNA for M4 muscarinic receptor
11365	23176	36403	3.3	3.8E+00	Y18000.1	NT	Homo sapiens NF2 gene
2635	15347		0.9	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6287	19070	32054	0.86	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN M10395
6873	19550	32626	0.86	3.8E+00	AI493849.1	EST_HUMAN	q25107.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2030437 3'
8331	21024	34161	1.1	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
8694	22345		0.62	3.8E+00	AJ380961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
4001	16748	29379	12.29	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7068	19757		1.03	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8609	21301		0.55	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
8078	21765	34928	0.7	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11408	24057	37363	2.23	3.7E+00	BF669278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11408	24057	37364	2.23	3.7E+00	BF669278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
578	13359	25986	5.19	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4745	17477		1.08	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
5174	17983	30498	0.74	3.6E+00	BF316316.1	EST_HUMAN	601801866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
8450	21142	34280	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone b08
8450	21142	34281	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone b08
8543	21235	34378	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8543	21235	34379	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gfpE), the translation start site has been verified (gfpC), and repressor protein (gfpR) genes, complete cds
10759	23444		4.07	3.6E+00	M96795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3241	16003	28852	1.1	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
5911	18695		1.17	3.5E+00	L42898.1	NT	
6118	18896	31894	1.18	3.5E+00	R19745.1	EST_HUMAN	y840c08.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
8383	21076		0.56	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
							zp86b04.s1 Strabagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8930	21621	34763	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Strabagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8930	21621	34764	1.02	3.5E+00	AA190998.1	EST_HUMAN	contains Alu repetitive element; contains element MSR1 repetitive element;
9393	22055	35227	0.96	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10417	23063	36283	0.48	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1501	14247	28633	2.94	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
7261	18945	33021	2.64	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7601	20267	33374	0.69	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8577	21269		0.7	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
8972	21662	34813	0.67	3.4E+00	AJ229042.1	NT	Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9010	21700	34850	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10164	22812	36030	2.97	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11519	24119	37429	1.89	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
5977	18759	31722	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
5977	18759	31723	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7764	20489	33611	0.79	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	23008	36223	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	23008	36224	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
483	13273	26208	1.64	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4004	13273	26208	0.9	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4679	17413	30048	1.08	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5481	18280	31176	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5481	18280	31177	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5515	18313	31214	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5515	18313	31215	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6214	18988	31984	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6214	18988	31985	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7505	20176	33270	0.7	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7672	20336	33448	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes
7672	20336	33449	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8928	21619		4.51	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9430	22108	35283	0.87	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (ILV1) gene, complete cds
10041	22689	35907	2.03	3.2E+00	AB016081.2	NT	Oryzias latipes OIG08 gene for guanylyl cyclase C, complete cds
11948	24500		2.44	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5785	18576	31505	2.46	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7287	19970	33047	0.93	3.1E+00	P62178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (C1PT)

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7627	20293		0.94	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
7986	20881	33807	0.48	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8500	21192	34333	4.36	3.1E+00	P48894	SWISSPROT	TYPE I IODOETHYRINE DEIODINASE (TYPE I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
8500	21192	34334	4.38	3.1E+00	P48894	SWISSPROT	TYPE I IODOETHYRINE DEIODINASE (TYPE I 6'DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
9168	21889		3.85	3.1E+00	Q14957	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9796	22447	35652	0.59	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
9888	22538		0.83	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 58.3 KD PROTEIN F52C8.5 IN CHROMOSOME III
10234	22882	36096	5.52	3.1E+00	P48365	SWISSPROT	DEOXYHYPOSINE SYNTHASE (DHS)
11440	23207		2.66	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] retinotic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-VZ1, mRNA, 2971 nt]
11463	24066		3.28	3.1E+00	S56680.1	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
2842	15610	28259	1.09	3.0E+00	8923984	NT	S. aureus genes encoding Sau981 DNA methyltransferase and Sau961 restriction endonuclease
6254	18090	30689	1.32	3.0E+00	X53096.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6461	19228	32228	0.83	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6461	19228	32228	0.83	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7055	19746		8.09	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7056	19785		0.6	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8805	21497		1.2	3.0E+00	X87638.1	NT	B. napus DNA for myosinase
10182	22840	36055	0.62	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYL TRANSFERASE) (ADOMET SYNTHETASE)
10544	23240	36474	1.57	3.0E+00	Q16181	SWISSPROT	GDC10 PROTEIN HOMOLOG
10531	23611	36960	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10331	23611	36961	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11578	24177	37492	2.72	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2004	14740	27464	2.28	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
6809	19470	32493	1.74	2.9E+00	Z36879.1	NT	F. pingid gdcPA gene for P-protein of the glycine cleavage system
7110	19798	32881	5.21	2.9E+00	Q14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7110	19788	32862	5.21	2.9E+00	Q14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7356	20037	33115	6.84	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7767	20463	33587	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7767	20463	33588	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7966	20691	33819	1.03	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4163059 5'
1440	14187	26872	4.4	2.8E+00	AF186398.1	NT	Buxus harlandii malic acid decarboxylase K (malK) gene, partial cds; chloroplast product
1620	14375		2.74	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7207	19892	32968	6.72	2.8E+00	8393724	NT	Mus musculus endomucin (LOC83423), mRNA
9513	22166		0.54	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10588	19892	32968	1.32	2.8E+00	8393724	NT	Mus musculus endomucin (LOC83423), mRNA
224	13036	25672	13.51	2.7E+00	6678306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
224	13036	25673	13.51	2.7E+00	6678306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5484	18263	31154	1.17	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kingle IV gene, exons 1 and 2
8045	20739		0.6	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8897	21558		1.83	2.7E+00	AL118459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9332	20403	33519	0.73	2.7E+00	AW088101.1	EST_HUMAN	xx88e12.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2691374 3' similar to gb:M17793
10397	23043		1.75	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4626	17361	28994	6.15	2.6E+00	AF068749.1	NT	CM0-BT0281-031199-087-H04 BT0281 Homo sapiens cDNA
5460	18259	31149	1.68	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5460	18259	31150	1.68	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5736	18528		0.58	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7454	25424		0.82	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7600	20266		0.04	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
7658	20653	33776	1.13	2.6E+00	AJ132180.1	NT	Mus musculus SH-2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
7958	20653	33777	1.13	2.6E+00	AJ132180.1	NT	Faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
8957	22210	35395	2.83	2.6E+00	AL161540.2	NT	Faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
10253	22901		1.67	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10553	23630	36878	1.32	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12580	25304		3.17	2.6E+00	11418220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1448	14195	26878	3.73	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
						NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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1448	14195	26879	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans racQ gene for DNA helicase, exons 1-4
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5723	18515	31435	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18516	31434	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18515	31435	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6030	18392	32406	0.64	2.5E+00	D30062.1	NT	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
7859	20323	33431	0.88	2.5E+00	AW040158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7700	20363	33477	0.68	2.5E+00	4502802	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9001	21691	34841	1.63	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9752	22403	35608	0.67	2.5E+00	BE287758.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531080 5'
11528	24128		1.34	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
11943	24498		3.08	2.5E+00	AF289635.1	NT	Mus musculus EIF-4I gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3012	15778	28428	1.13	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4849	17579	30203	6.09	2.4E+00		SWISSPROT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5920	18705	31557	4.18	2.4E+00	P02843	EST_HUMAN	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7280	18964	33040	0.78	2.4E+00	BF687502.1	EST_HUMAN	602120858F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7280	18964	33041	0.78	2.4E+00	BF687502.1	EST_HUMAN	602120858F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
8039	20734	33885	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8039	20734	33886	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8110	20804		2.63	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J59 section 47 of 132 of the complete genome
8549	21241		1.61	2.4E+00	AW875128.1	EST_HUMAN	RC2-PT0004-031298-011-c05 PT0004 Homo sapiens cDNA
8727	21419	34563	7.36	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9838	22586	35788	2.66	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9838	22586	35789	2.66	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10007	22655	35868	1.86	2.4E+00	X02511.1	NT	H.sapiens CTGF gene and promoter region
10143	22791		6.55	2.4E+00	P09089	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10220	22868	36079	1.62	2.4E+00	BE326702.1	EST_HUMAN	h63f06.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3133187 3'
10220	22868	36080	1.62	2.4E+00	BE326702.1	EST_HUMAN	h63f06.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3133187 3'
10460	23136	36364	0.87	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11331	24022	37327	2.16	2.4E+00	AF158632.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1231	13980	26660	13.6	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4102	16845		1.35	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5744	18536		0.95	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7354	20035	33113	2.47	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7495	25425		3.07	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7679	20343	33455	1.01	2.3E+00	X60265.1	NT	M.mazal dnaK and dnaJ genes homologues coding for DnaK and DnaJ
8008	21698	34849	0.54	2.3E+00	5836317	NT	Polyturus ornaticornis mitochondrion, complete genome
8088	21757	34919	1.8	2.3E+00	Q11127	SWISSPROT	ALPHA-(1-3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10704	23396	36832	3.83	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11782	24373	37703	3.03	2.3E+00	BF541987.1	EST_HUMAN	60206812F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11782	24373	37704	3.03	2.3E+00	BF541987.1	EST_HUMAN	60206812F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12157	24642	37099	6.84	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
3698	16746	29378	0.95	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4278	17017	29844	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4278	17017	29845	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5258	18064	30692	12.73	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)(>
5258	18064	30693	12.73	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11)(>
5763	18554	31478	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
5763	18554	31479	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
5971	18753	31714	9.84	2.2E+00	BE260383.1	EST_HUMAN	60094340T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6261	19035	32010	3.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6502	19267	32269	3.16	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6881	17938		3.94	2.2E+00	AA694574.1	EST_HUMAN	nB5502.s1 NC1_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7217	19002	32975	0.9	2.2E+00	AA137027.1	EST_HUMAN	zr97704.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:666143 5'
7507	20178	33272	19.2	2.2E+00	AA449012.1	EST_HUMAN	z05g10.r1 Soares fetal Nb21f8_9w Homo sapiens cDNA clone IMAGE:785634 5'
7589	20257	33365	0.72	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8001	20696	33823	0.58	2.2E+00	BE301560.1	EST_HUMAN	b017h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8001	20698	33824	0.58	2.2E+00	BE301580.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8241	21920		11.02	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9468	25124		2.28	2.2E+00	Q04706	SWISSPROT	TRANSPOSON TY1 PROTEIN A
9953	22601	35804	1.1	2.2E+00	A1280373.1	EST_HUMAN	qm68b03.x1 Soares placenta_8to9weeks_2NbHP80c9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
9953	22601	35905	1.1	2.2E+00	A1280373.1	EST_HUMAN	qm68b03.x1 Soares placenta_8to9weeks_2NbHP80c9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
9998	22844	35958	2.68	2.2E+00	BF246782.1	EST_HUMAN	601855581F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10353	23000	36217	3.11	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11418	23185	36415	3.47	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11616	24214	37639	5.89	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
558	15545	25967	8.3	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3575	16330		1.08	2.1E+00	AW449388.1	EST_HUMAN	U1H-B13-ak-e-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734560 3'
6041	16821		0.89	2.1E+00	P76357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6710	16625	32989	3.95	2.1E+00	O70159	SWISSPROT	ALPHA-2 HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6846	19428	32443	5.72	2.1E+00	N29576.1	EST_HUMAN	W08a10.s1 Soares melanocyte 2NbIM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M56854 TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
8395	21098		1.97	2.1E+00	AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1174	13927	26591	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1174	13927	26592	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1312	14060	26735	0.97	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
1569	14316		2.61	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYL TRANSFERASE SPB1
2145	14875	27809	5.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2145	14875	27810	5.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4080	18824	29450	2.2	2.0E+00	AW684498.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4080	18824	29451	2.2	2.0E+00	AW684498.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7449	20125		0.82	2.0E+00	P07566	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7923	20618	33745	3.17	2.0E+00	AB008678.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7923	20618	33746	3.17	2.0E+00	AB008678.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7923	20618	33747	3.17	2.0E+00	AB008678.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8820	21512	34656	3.15	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12481	26285	30720	7.27	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5511	18309	31209	4.77	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itpr1), mRNA
5511	18308	31210	4.77	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itpr1), mRNA
6009	18780	31763	1.32	1.9E+00	BE969895.1	EST_HUMAN	601678636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6556	19321		0.75	1.9E+00	AW845889.1	EST_HUMAN	MRO-CT0063-071098-002-g02 CT0063 Homo sapiens cDNA
6650	19412		2.46	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8358	21051	34180	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8358	21051	34191	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8557	21249		2.94	1.9E+00	BF380206.1	EST_HUMAN	OM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
8792	21484		1.33	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
8930	22183	35387	0.69	1.9E+00	AA669125.1	EST_HUMAN	ab94a04.s1 Stragane lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element/contains element L1 L1 repetitive element ;
10462	23108	30339	0.62	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pod precursor protein gene, partial cds
3088	15854	28408	1.3	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3118	15883	28522	1.57	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3118	15883	28523	1.57	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5771	18568		1.91	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6013	18794	31757	1.32	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6305	19077		1.12	1.8E+00	BF883327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:428272 5'
6841	19403	32418	1.64	1.8E+00	BF305952.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
6958	19440	32455	1.79	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8016	20711	33841	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8016	20711	33842	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8368	21061	34201	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34202	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34203	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8753	21445	34593	1.98	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9073	21762	34924	0.77	1.8E+00	R31042.1	EST_HUMAN	yt72c08.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9161	21831	34994	0.76	1.8E+00	AW880004.1	EST_HUMAN	QV0-O10030-070300-148-ab03 OT0030 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9749	22400	35605	0.75	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22831		3.2	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10452	23098		0.63	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12278	25238		5.29	1.8E+00	AF314264.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12359	24763		3.9	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpct1b), mRNA
1086	13844	26502	2.21	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2269	14995	27734	2.29	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21Q080
2372	15094	27833	2.66	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4428	17182	29782	0.81	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5525	18323	31223	1.77	1.7E+00	BE063546.1	EST_HUMAN	CMD-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
5525	18323	31224	1.77	1.7E+00	BE063546.1	EST_HUMAN	CMD-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
5927	18711	31686	3.28	1.7E+00	Q9TTR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
7118	19808	32871	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7118	19808	32872	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7763	20449	33573	0.91	1.7E+00	AF021836.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7932	20627	33755	1.13	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tcl1), mRNA
7981	20656	33781	0.59	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214869 5'
8440	21132	34268	0.5	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus Interferon Inducible Mx protein (Mx) mRNA, complete cds
8525	21217		2.3	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8605	21297	34440	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for ankyrin
8605	21297	34441	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for ankyrin
9047	25123	34892	2.18	1.7E+00	Q60478	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9047	25123	34893	2.18	1.7E+00	Q60478	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9506	22159		1.15	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10071	22719		0.48	1.7E+00	AW953881.1	EST_HUMAN	EST365761 MAGE resequences, MAGC Homo sapiens cDNA
11508	24195	37514	2.57	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp5098-cleaved sublibrary Homo sapiens cDNA not directional
12231	24684	31074	1.9	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.1
12717	24990	30970	1.84	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element; qf50b01.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 repetitive element;
2027	14782	27491	18.51	1.6E+00	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

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2036	14771	27500	3.75	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2042	14776	27505	1.54	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2282	15007		1.24	1.6E+00	X98373.1	NT	B. napus gene encoding endo-polygalacturonase
2881	15727	28377	1.61	1.6E+00	W58428.1	EST_HUMAN	zid25f01.1 Scores_fetal_heart_Nb1H19W Homo sapiens cDNA clone IMAGE:341688 5' similar to gib:D28805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
4011	16757		5.68	1.6E+00	BF570077.1	EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4319	17058	29682	1.9	1.6E+00	AF159827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4319	17058	29683	1.9	1.6E+00	AF159827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4942	17669	30277	0.84	1.6E+00	AF075394.1	NT	Urothuchis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
4942	17669	30278	0.84	1.6E+00	AF075394.1	NT	Urothuchis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5024	17745	30356	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5024	17745	30357	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5737	18529	31450	2.16	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end
5823	18612	31543	0.79	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6378	19147	32146	0.69	1.6E+00	BF380703.1	EST_HUMAN	IL2-JT0073-060800-145-E02 UT0073 Homo sapiens cDNA
6810	19373	32387	1.06	1.6E+00	AW294881.1	EST_HUMAN	U1H-B12-ahr-b-04-Q-UJ.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7145	19832	32901	2.73	1.6E+00	BE697267.1	EST_HUMAN	RCO-CT0416-200700-032-c10 CT0416 Homo sapiens cDNA
7828	20624		1.19	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8277	20671	34112	3.28	1.6E+00	AJ297131.1	NT	Mus musculus S1L, MAP_17, CYP_a, SCL & CYP_b genes
8798	21490	34636	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8798	21490	34637	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8970	21680	34810	0.47	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9360	25121	33549	1.94	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9360	25121	33550	1.94	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9487	22140		0.56	1.6E+00	AF043466.1	NT	Thermococcus ethanolicus D-xylose-binding protein (xylF) gene, complete cds
9634	22286	35480	1.32	1.6E+00	T41280.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primered hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
10047	22695	35911	0.5	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lai (IAL), and zinc finger protein (DNZ1) genes, complete cds
10085	22733	35947	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0018-080200-100-d07 LT0018 Homo sapiens cDNA
10085	22733	35948	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0018-080200-100-d07 LT0018 Homo sapiens cDNA
10242	22890	36102	0.47	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10491	23137	36365	0.45	1.6E+00	AF162084.1	NT	Glucose glucosyl beta-tubulin 2 (tubub2) gene, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10670	23361	36602	1.95	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10728	23416	36657	1.27	1.6E+00	AA216387.1	EST_HUMAN	nc168402.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008267 similar to contains element MER4 repetitive element;
10747	18612	31643	5.27	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
11705	24300	37626	3.46	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
31	12859	25476	5.31	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
225	13037	25674	2.2	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AF39, section 32 of 94 of the complete genome
608	13394						Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardin) (Adam15), mRNA
2410	15131	27867	1.95	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2519	15235	27975	2	1.5E+00	6676350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3135	15131	27867	1.85	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3368	16127	28785	0.72	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5642	18437	31350	0.83	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1;
5642	18437	31351	0.83	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1;
6312	19083	32068	3.02	1.5E+00	R17879.1	EST_HUMAN	y010e02.f1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7028	19720		1.37	1.5E+00	BE785356.1	EST_HUMAN	801478745f.1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7060	19751	32814	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7060	19751	32815	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7245	18930	33006	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak20f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7463	20165	33257	0.76	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Stratiotes schizoid brain S11 Homo sapiens cDNA clone IMAGE:1684683 3' similar to gb:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN);
7727	20390		0.64	1.5E+00	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8021	20716	33548	0.89	1.5E+00	BE987446.1	EST_HUMAN	601509586f1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8542	21234	34377	0.84	1.5E+00	K02138.1	NT	Mouse gamma1 IgM chain gene, mu-delta region
8914	21605		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hCGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9032	21722	34678	0.46	1.5E+00	BF217818.1	EST_HUMAN	601882662f1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086135 5'
9383	22045	35217	0.64	1.5E+00	R81928.1	EST_HUMAN	y03h01.f1 Soares placenta Nb21P Homo sapiens cDNA clone IMAGE:147697 5'
9535	22168	35374	1.39	1.5E+00	AW375697.1	EST_HUMAN	QV3-GT0182-261089-008-008 GT0182 Homo sapiens cDNA
9780	22411	35618	6.39	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
9952	22600		1.77	1.5E+00	BF337944.1	EST_HUMAN	602035771f1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183865 5'
10096	22744	35958	1.68	1.5E+00	AA017689.1	EST_HUMAN	z83g06.f1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361308 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10056	22744	35959	1.86	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.f1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:361306 5'
11375	23982	37282	4.46	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243.s1 547 (synonym: hifb1) Homo sapiens cDNA clone DKFZp547P243 3'
11530	24130		6.55	1.5E+00	X07380.1	NT	Maize mitochondrial rRNA-Ser gene and rRNA-Phe pseudogene
11629	24228	37549	2.1	1.5E+00	AI400798.1	EST_HUMAN	ig94d09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11628	24228	37550	2.1	1.5E+00	AI400798.1	EST_HUMAN	ig94d09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12222	25325	30713	1.44	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12445	24815		3.38	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
28	12856	25472	2.76	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
28	12856	25473	2.76	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2333	18057		6.92	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2675	15384	28125	2.21	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2776	15461	28221	2.61	1.4E+00	AF084564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2776	15461	28222	2.61	1.4E+00	AF084564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4545	17280		1.81	1.4E+00	BF681547.1	EST_HUMAN	602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297558 5'
5288	18093	30754	1.61	1.4E+00	AW054976.1	EST_HUMAN	w45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5441	18240		5.57	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6186	18963	31936	2.72	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6202	25420		4.02	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6318	18089	32074	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	18089	32075	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
7188	19872	32946	2.07	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7201	19887	32962	1.17	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2819673 3' similar to contains Alu repetitive element
7258	19942	33018	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7258	19942	33019	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8233	20927		0.68	1.4E+00	P07693	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8693	21385		4.47	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8991	21681	34829	1.73	1.4E+00	R20459.1	EST_HUMAN	y933f12.f1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34945 5'
9097	21785	34951	4.65	1.4E+00	BE064667.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9131	21819	34985	0.51	1.4E+00	AF134944.1	NT	Scoloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10108	22756	35898	0.79	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10151	22789	38015	0.81	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10151	22788	38016	0.81	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10424	23070	38281	1.08	1.4E+00	D63441.1	NT	Pandorina colimariensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10424	23070	38282	1.06	1.4E+00	D63441.1	NT	Pandorina colimariensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11003	23675	36931	1.34	1.4E+00	AA195528.1	EST_HUMAN	z38609.r1 Soares NIH-MP_Pu_S1 Homo sapiens cDNA clone IMAGE:686512 5' similar to contains element
11188	23853	37139	6.16	1.4E+00	AB006882.1	NT	MER22 repetitive element;
11381	23988	37288	4.42	1.4E+00	BE982107.2	EST_HUMAN	Homo sapiens APEGED mRNA for AIRE-1, complete cds
11381	23988	37289	4.42	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37357	3.46	1.4E+00	U30790.1	NT	601655184R1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37358	3.46	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12079	25256		1.48	1.4E+00	AL161500.2	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
567	13339		1.81	1.3E+00	Z79640.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
882	13651	26320	3.42	1.3E+00	AJ271192.1	NT	M.mucedo gene encoding 4-Dihydroxyethyl-trispartate dehydrogenase
1107	13884		20.26	1.3E+00	Y19213.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1274	14024	26882	13.71	1.3E+00	4507898	NT	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
1274	14024	26893	13.71	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	14083		1.26	1.3E+00	U61730.2	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1605	14351		2.27	1.3E+00	AE002238.2	NT	Cox lacryna-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
2239	14987		1	1.3E+00	AB030447.1	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2405	15126	27862	1.27	1.3E+00	P23391	SWISSPROT	Cyprinus carpio MRPB and MASPB genes for mannose-binding lectin-associated serine protease (MASP) and MASPB-related protein, complete cds
2853	15288		1.75	1.3E+00	BE966735.2	EST_HUMAN	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2940	15705	28354	0.73	1.3E+00	6755621	NT	601681233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915946 3'
3684	18338	28864	0.89	1.3E+00	AF016494.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
5427	18226	30338	1.08	1.3E+00	P19732	SWISSPROT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P66), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-protease enhancer protein (PCOLCE) genes, complete c>
5622	18418	31330	0.61	1.3E+00	M27138.1	NT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5853	18650	31590	0.81	1.3E+00	BF663925.1	EST_HUMAN	Human estradiol 17 beta-dehydrogenase gene, complete cds
5828	18712	31687	7.57	1.3E+00	AW362834.1	EST_HUMAN	602145284F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309085 5'
							PMO-CT0289-291189-004-008 CT0289 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5928	18712	31658	7.57	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0288-281189-004-f08 CT0289 Homo sapiens cDNA
6323	18093	32081	1.34	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6652	19414		0.75	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6739	19573	32006	0.82	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
6854	19554	32594	1.17	1.3E+00	BE538818.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7000	19692	32743	0.81	1.3E+00	BE249571.1	EST_HUMAN	TCBAP1D0859 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0859
7358	20039	33117	1.01	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8197	20891	34029	1.28	1.3E+00	AJ009812.1	NT	Sus scrofa pip gene
8346	21039	34176	2.78	1.3E+00	BE863379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866185 3'
8459	21151	34294	0.86	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8611	21303		1.78	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8989	21381	34525	0.79	1.3E+00	A827628.1	EST_HUMAN	wc85a07.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9415	22093		5.24	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9424	22102	35273	2.56	1.3E+00	X72018.1	NT	S.alba phr-1 mRNA for photolyase
9424	22102	35274	2.56	1.3E+00	X72018.1	NT	S.alba phr-1 mRNA for photolyase
9524	22177	35361	0.96	1.3E+00	AF059250.1	NT	Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds
9589	22222	35407	1.56	1.3E+00	Q00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9651	22303	35408	1.14	1.3E+00	A1927628.1	EST_HUMAN	wc85a07.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9726	22377	35576	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-1191 chromosomal inversion junction DNA
9726	22377	35579	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-1191 chromosomal inversion junction DNA
9766	22417	35624	4.53	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866185 3'
9828	22477		0.48	1.3E+00	A1559944.1	EST_HUMAN	1q77a12.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:U14723
10050	22698	35913	0.46	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10050	22698	35914	0.46	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10113	22761	35974	1.62	1.3E+00	A5004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10130	22778	35991	1.35	1.3E+00	M29953.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10483	23129		0.82	1.3E+00	AL163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10511	23157	36383	0.45	1.3E+00	A1980846.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
10592	23286		4.6	1.3E+00	Q14117	SWISSPROT	wc32a10.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2468922 3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE ;
							DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)

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Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10822	23505	36744	1.93	1.3E+00	P25299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10846	23528	36772	2.01	1.3E+00	Z18922.2	NT	Mus musculus desmin gene
11307	23666		1.8	1.3E+00	AW274791.1	EST_HUMAN	xp09e03.x1 NCJ CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11527	24127	37433	3.21	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11624	24221	37544	3.16	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.8kb fragment
12210	24675		2.64	1.3E+00	AF187878.1	NT	Cavia porcellus inwardly-rectifying potassium channel KJ2.2 (KCNU12) gene, complete cds
12388	24780	31035	6.3	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCJ CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158452 5'
12397	25153		2.73	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12489	24848		2.15	1.3E+00	AF187035.1	NT	Stumra liliun cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
635	13414	26050	11.05	1.2E+00	AA676246.1	EST_HUMAN	Z122408.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431635 3'
804	13576	26239	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26240	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26241	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13627		1.36	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1138	13893	26554	5.64	1.2E+00	AF080245.2	NT	Elasit oleifera sesquiterpene synthase mRNA, complete cds
1183	13935	26600	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1183	13935	26601	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2003	14739	27463	1.22	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3108	15873	28512	1.24	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3163	15926	28573	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3163	15926	28574	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3250	16041		2.59	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3699	16452	29091	6.69	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3967	16716	29354	1.78	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4266	16710	28766	1.11	1.2E+00	AF189740.1	NT	Homo sapiens LHX3 gene, intron 2
4438	17174		1.57	1.2E+00	MB7080.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4487	17222	29850	0.86	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4523	17258	29892	1.89	1.2E+00	AF166495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4548	17283		6.43	1.2E+00	Y08200.1	NT	T. pinatum chloroplast rbcL gene, partial
5351	18154	30836	1.1	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5487	18266	31158	1.91	1.2E+00	AW813276.1	EST_HUMAN	MFR-STD191-140200-013-c05 ST0191 Homo sapiens cDNA
5784	18575	31504	0.83	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6060	18940	31801	2.51	1.2E+00	X74895.1	NT	D.hydrel a1 repeat cluster DNA, fragment D
6119	18997	31865	4.42	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6198	18974	31951	1.54	1.2E+00	X98084.1	NT	C.glutamicum pta gene and ackA gene
6198	18974	31952	1.54	1.2E+00	X98084.1	NT	C.glutamicum pta gene and ackA gene
6241	19015	31989	39.54	1.2E+00	AA758254.1	EST_HUMAN	ab84g12.s1 Scores_teste_NHT Homo sapiens cDNA clone 1322374 3'
6342	19112	32101	0.55	1.2E+00	N33295.1	EST_HUMAN	y39b12.s1 Scores melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:273599 3' similar to gb U87895 HUMALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6408	19177	32175	0.68	1.2E+00	P17671	SWISSPROT	ECODYSONE-INDUCIBLE PROTEIN E75-A
6412	19180	32179	2.06	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0181-140200-013-c05 ST0191 Homo sapiens cDNA
6815	19476	32498	1.17	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
6829	19490	32512	3.11	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7163	19840		0.94	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7282	25109	33044	4.86	1.2E+00	AV734565.1	EST_HUMAN	AV734565 cDNA Homo sapiens cDNA clone cDNAFFH03 5'
7550	20220	33323	2.49	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
7603	20269	33376	0.58	1.2E+00	J05218.1	NT	Chicken muscarinic acetylcholine receptor (m4 mAChR) gene, complete cds
7715	20379	33492	0.56	1.2E+00	BE787646.1	EST_HUMAN	601481781F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8487	21159	34302	3.32	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8561	21253	34391	0.68	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE
8775	21497		0.51	1.2E+00	7706271	NT	GLUCOSYL TRANSFERASE
8923	21614	34758	1.87	1.2E+00	AW377210.1	EST_HUMAN	Homo sapiens CGI-30 protein (LOC51611), mRNA
9138	21826	34991	0.5	1.2E+00	H48599.1	EST_HUMAN	MR2-CT0222-201089-001-e07 CT0222 Homo sapiens cDNA
9298	21965	35138	3.75	1.2E+00	Z32850.1	NT	y68a08.l1 Scores fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:202068 5'
9505	22158	35339	1.81	1.2E+00	D11745.1	EST_HUMAN	R.communis gene for pyrophosphate-dependent phosphotransferase beta subunit
9831	22482	35684	2.86	1.2E+00	X58832.1	NT	HUMHM07A01 Liver HepG2 cell line. Homo sapiens cDNA clone hrm01a01
10224	22872		0.73	1.2E+00	AB008666.1	NT	H.sapiens ENO3 gene for muscle specific enolase
11318	24009	37314	3.78	1.2E+00	AW817817.1	EST_HUMAN	Homo sapiens Kdtrr gene, exon 1
11357	24045		10.62	1.2E+00	BE160761.1	EST_HUMAN	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
11435	23202	36434	4.36	1.2E+00	U50147.1	NT	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
12179	25227	30817	17.08	1.2E+00	AL163203.2	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12199	24667		2.8	1.2E+00	AP001515.1	NT	Homo sapiens chromosome 21 segment HS21C003
451	13237	25876	1.53	1.1E+00	D86980.1	NT	Bacillus halodurans genomic DNA, section 9/14
1757	14499	27200	1.33	1.1E+00	AW095393.1	EST_HUMAN	Human mRNA for KIAA0227 gene, partial cds
1892	14828	27339	0.88	1.1E+00	AW157589.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
							UIHF-BR0p-ekf-02-0-U1.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3324	16084	28734	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3324	16084	28735	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3480	16236	28892	1.11	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3567	16322	28970	1.01	1.1E+00	AJ808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358461 3' similar to
3707	16460	29098	1.05	1.1E+00	AE003888.1	NT	SW:PS31_HUMAN Q12888 P53-BINDING PROTEIN 53BP1;
3707	16460	29099	1.05	1.1E+00	AE003888.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3788	16550		1.02	1.1E+00	X85374.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
4190	16831		5.69	1.1E+00	5836331	NT	H.parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4634	17369		0.81	1.1E+00	U34982.1	NT	R.uniconnis complete mitochondrial genome
4934	17682	30272	3.45	1.1E+00	U18466.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
4935	17683	30273	1.06	1.1E+00	AJ271740.1	NT	African swine fever virus, complete genome
5129	17847	30464	1.07	1.1E+00	6680080	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5224	18031	30657	1.39	1.1E+00	6978530	NT	Homo sapiens putative GR6 protein (GR6), mRNA
5526	18324	31226	16.76	1.1E+00	BE960184.1	EST_HUMAN	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5545	18342	31260	1.2	1.1E+00	AJ136882.1	EST_HUMAN	601652776R1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3825835 3'
6001	18782	31743	1.1	1.1E+00	11419739	NT	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738260 3'
6181	18956	31932	0.82	1.1E+00	AF197881.1	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6313	19084	32069	0.82	1.1E+00	R06037.1	EST_HUMAN	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6616	19379	32394	0.72	1.1E+00	AJ404004.1	NT	ye89e03.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:124924 5'
7155	19842	32956	0.98	1.1E+00	AF101081.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7196	19882	32958	0.72	1.1E+00	X55681.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7369	20068	33146	2.18	1.1E+00	Z72338.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7369	20068	33147	2.18	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7411	20086	33172	8.94	1.1E+00	AL161588.2	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7480	25115	33247	0.8	1.1E+00	11967860	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8032	20727	33860	3.01	1.1E+00	BF633986.1	EST_HUMAN	Mus musculus eilant mating type information regulation 2, (S.carevisiae, homolog) like (Sir2), mRNA
8120	20814	33950	0.64	1.1E+00	AF478339.1	EST_HUMAN	602082582F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4246828 5'
8636	21326	34471	0.71	1.1E+00	AB003088.1	NT	Im38h11.x1 NCL_CGAP_KJH11 Homo sapiens cDNA clone IMAGE:2160549 3'
8714	21406	34549	0.75	1.1E+00	S80750.1	NT	Acetabularia calliculus mitochondrial COX-like gene
							VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 376
							nt]

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8824	21516	34661	0.45	1.1E+00	AI078946.1	EST_HUMAN	α2405.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9337	20408		0.69	1.1E+00	BE384876.1	EST_HUMAN	80127/6278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9528	22181	35365	0.63	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9580	22233		1.2	1.1E+00	Y1227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9672	22324	35520	1.14	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
9732	22383	35585	1.37	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
9837	22488	35680	4.59	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9898	22548	35742	18.34	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10398	23044	36260	1.1	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10504	23150	36375	0.73	1.1E+00	AI878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5' similar to gb:D10522
10547	23243	36478	2.25	1.1E+00	11067364	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN);
10606	23300		3.1	1.1E+00	AF068942.1	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
11023	23695	36958	1.28	1.1E+00	11439596	NT	Klebsiella fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11026	23698	36961	1.58	1.1E+00	L16877.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11042	17901		5.23	1.1E+00	8922973	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11048	23718	36988	3.68	1.1E+00	AF012662.1	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11048	23718	36989	3.68	1.1E+00	AF012662.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11328	24018	37323	4.58	1.1E+00	AB09689.1	EST_HUMAN	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11561	24160	37470	1.63	1.1E+00	D89501.1	NT	wf76e11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2381548 3'
11581	24160	37471	1.63	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12153	24639		3.66	1.1E+00	P07866	SWISSPROT	Human PBI gene, complete cds
12250	24697	31078	1.93	1.1E+00	AF216698.1	NT	LOW TEMPERATURE ESSENTIAL PROTEIN
12378	25225		2.09	1.1E+00	AF234169.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12388	25200		1.44	1.1E+00	8393198	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
97	12923		2.46	1.0E+00	U23808.1	NT	Rattus norvegicus C-reactive protein, member of the pentraxin family (Cp), mRNA
111	12932	25569	0.73	1.0E+00	D88425.1	NT	Xenopus laevis rhodopsin gene, complete cds
409	13194		2.25	1.0E+00	AB021684.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
562	13344	25971	1.2	1.0E+00	AJ251680.1	NT	Marchantia polymorpha genes for 26S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
662	13438	26079	4.38	1.0E+00	AL163218.2	NT	Giardia lignina mRNA for homeodomain transcription factor (so gene)
						NT	Homo sapiens chromosome 21 segment HS21C018

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663	13439		0.95	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1365	15567		3.03	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1751	14493	27163	0.93	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural
2489	15206	27947	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2489	15206	27948	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2878	15645	28287	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2878	15645	28288	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2867	15793		1.17	1.0E+00	O14228	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME I
3194	15957	28609	1.24	1.0E+00	AA628453.1	EST_HUMAN	af28g08.s1 Soares_total_fetus_Nb2HF8_pw Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3595	12923		1.24	1.0E+00	U23808.1	NT	WP-C42D8.3 CE04204 :contains element MER22 MER22 repetitive element ;
3669	16422	28063	1.04	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4050	16795	29424	0.76	1.0E+00	AF223391.1	NT	Homo sapiens bisonus mRNA for tyrosinase
4242	16983		0.79	1.0E+00	8922245	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4954	17680		0.93	1.0E+00	D10852.1	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4975	17698	30306	0.74	1.0E+00	AF092505.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5200	18008	30628	3.53	1.0E+00	Z97022.1	NT	Mus musculus dipeptidyl aminopeptidase-like protein 6 (Dpp6) gene, partial cds; and proctinal Rump white inversion breakpoint
5759	18551	31472	4.97	1.0E+00	AF248054.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5759	18551		4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5769	18551	31473	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5867	18554	31595	1.53	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6
6024	18804	31765	4.7	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6030	18810	31770	1.49	1.0E+00	AW452782.1	EST_HUMAN	UIH-B13-abx-4-09-Q-UI.s1 NCI_CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6097	19168	32168	1.95	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6447	18215	32213	0.91	1.0E+00	AF104688.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6534	18300		1.08	1.0E+00	P48506	SWISSPROT	SRB-11 PROTEIN
6679	18596	32634	1.33	1.0E+00	Y11204.1	NT	V. carteri gene encoding vdwocapsin

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7038	19730	32788	1.09	1.0E+00	S52770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7378	20058			1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7611	20277	33385	9.29	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7626	20282	33401	5.26	1.0E+00	AA775191.1	EST_HUMAN	ec76b08.s1 Stratiene lung (#37210) Homo sapiens cDNA clone IMAGE:868791 3'
7861	20556	33681	1.36	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848006 5'
7861	20556	33682	1.36	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848006 5'
8041	17680		1.19	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8248	20942	34078	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8248	20942	34080	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8378	21069		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8408	21101	34237	0.5	1.0E+00	Q8Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8408	21101	34238	0.5	1.0E+00	Q8Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8436	25122		2.34	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181089-011-008 HT0229 Homo sapiens cDNA
8476	21169	34312	0.88	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8625	21317	34459	1.27	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9171	21841	35006	2.43	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889421 5'
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9510	22163	35345	1.83	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9516	22169	35351	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xzPC) mRNA, complete cds
9516	22169	35352	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xzPC) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9753	22404	35609	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9753	22404	35610	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10012	22660	35876	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10012	22660	35876	0.71	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10104	22752	35966	0.81	1.0E+00	A1077920.1	EST_HUMAN	cy15d07.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10225	22873	36085	4.36	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'
10375	23021	36237	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10375	23021	36238	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10407	23053	38270	1.1	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10893	23573	36823	4.57	1.0E+00	S90825.1	NT	PBR1-proline-rich protein (intron 3) [human, Genomic, 898 nt]
11025	23697	36960	1.49	1.0E+00	AA701494.1	EST_HUMAN	zh63b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Abu repetitive element; contains element MER38 repetitive element;
11522	24122		1.59	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
11744	18008	30628	1.55	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine protease
11838	24422	37763	12.29	1.0E+00	Q60019	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8 (NADH DEHYDROGENASE 1, CHAIN 8) (NDH-1, CHAIN 8)
11868	24452	37764	1.38	1.0E+00	9826187	NT	Human adenovirus type 5, complete genome
12049	24568		3.01	1.0E+00	P15308	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12370	24772		2.32	1.0E+00	AW976184.1	EST_HUMAN	EST398283 MAGE resequences, MAGN Homo sapiens cDNA
2643	15353	28097	1.19	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3591	16345		0.97	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5547	18344	31253	10.09	9.8E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
5779	18570	31498	0.93	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9160	21830		1.37	9.9E-01	U65667.1	NT	Lycopodium obscurum putative M1 copy 1 nematode-resistance gene
9455	22005		2.18	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10814	23308	36547	2.37	9.9E-01	AJ005028.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rit6
11592	24191	37508	2.3	9.9E-01	Y11972.1	NT	B.aphidicola 16S rDNA (host T. subter)
11692	24191	37509	2.3	9.9E-01	Y11972.1	NT	B.aphidicola 16S rDNA (host T. subter)
510	13294	25926	1.14	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2295	15020		1.21	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2804	15509		1.01	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3781	16533	29171	0.92	9.8E-01	O67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEONUCLEASE IV)
7069	19786	32852	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7099	19788	32853	4.87	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7545	20215	33316	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7646	20215	33317	1.16	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
8619	21311	34453	0.91	9.8E-01	FP38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10336	22983		1.13	9.8E-01	AA825565.1	EST_HUMAN	cd55304.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
10916	23596	36842	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360760 5'
10916	23596	36843	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360760 5'
11764	24355	37698	1.57	9.8E-01	AF680876.1	EST_HUMAN	b42c10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12256	24702		1.56	9.8E-01	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca ²⁺ /Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7058	19749	32812	2.28	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8401	21094	34230	1.68	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8407	21100	34236	1.3	9.7E-01	M80544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
11123	23782		3.84	9.7E-01	BF511209.1	EST_HUMAN	UH-HB4-ec-e-07-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
4425	17161	29791	1.5	9.6E-01	AW799874.1	EST_HUMAN	PM2-UJM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5667	18482	31376	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5667	18482	31377	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6848	19410	32424	0.61	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8291	20985		2.33	9.6E-01	X96275.1	NT	P.falciparum complete gene map of plastid-like DNA (IR-A)
8750	21442	34589	0.59	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
11503	24104	37416	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPOBAG06 5'
11503	24104	37417	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPOBAG06 5'
11952	24505		1.92	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12558	25301	30710	2.18	9.6E-01	U91423.1	NT	Sphynx fibro NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2480	16198	27838	1.05	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2673	15382	28122	0.97	9.5E-01	Q02934	SWISSPROT	ENDOGLUCANASE [PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULOSE I)]
3762	16514	28150	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3762	16514	28161	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8899	21590	34730	0.69	9.5E-01	AI180182.1	EST_HUMAN	q57407.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9003	21693	34843	1.05	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0285-241189-011-b02 CT0285 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11209	23872	37159	1.88	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103830 5'
11429	23186	36427	2.42	9.5E-01	AW283789.1	EST_HUMAN	UHH-B12-arp-f-03-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
11795	24385	37718	1.55	9.5E-01	T67204.1	EST_HUMAN	ye53d04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66631 3'
3196	15959		3.33	9.4E-01	AF166990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (pob) gene, partial cds
3212	15975		2.06	9.4E-01	AF080595.1	NT	Plinipirella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8764	21456	34808	0.87	9.4E-01	M80724.1	NT	Human Fe-gamma-receptorIIA (FCGR2A) gene, exon 4
12202	24670		1.92	9.4E-01	BE781251.1	EST_HUMAN	601468703F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3869828 5'
12557	25219		1.79	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1728	14468		1.05	9.3E-01	AF242382.1	NT	Homo sapiens phytoyl-CoA hydratase (PHYH) gene, exon 5
2640	15351	28095	1.36	9.3E-01	BE071172.1	EST_HUMAN	RC5-BTD503-271189-011-B01 BTD503 Homo sapiens cDNA
4015	16761	29388	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4015	16761	29389	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5805	18303	31204	1.56	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5592	18398	31298	3.89	9.3E-01	L39189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7868	20691	33785	1.65	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
8713	21405		1.04	9.3E-01	AF061891.1	NT	Xenopus laevis CCCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8835	21527	34673	0.95	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12681	24970		3.12	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), callitradin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
12802	25049		1.48	9.3E-01	U82671.2	NT	
3233	15995	28848	2.93	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4822	17653		0.97	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5831	18428		1.15	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
5898	18683	31631	7.36	9.2E-01	BF037698.1	EST_HUMAN	601461153F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3864661 5'
6837	19302	32306	0.61	9.2E-01	M84703.1	NT	N.cassa valy-4RNA synthetase (cyl-20/un-3) gene
9660	22213	35399	0.92	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9848	22300	35498	1.07	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10165	22813	36031	3.16	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10315	22902	36178	1.9	9.2E-01	BF583251.1	EST_HUMAN	7058e06.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW_NU5M_TRYBB
10543	23239	38473	1.63	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH+UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11722	24316	37639	1.79	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1621	14368	27057	1.88	9.1E-01	T98876.1	EST_HUMAN	ye5201.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element;
2120	14851		2.78	9.1E-01	8823058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3200	15963	28614	1.15	9.1E-01	T28418.1	EST_HUMAN	AB200038R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200038 5'
3200	15963	28615	1.15	9.1E-01	T28418.1	EST_HUMAN	AB200038R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200038 5'
6075	18854	31821	1.28	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6413	18181	32180	3.53	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7475	20148	33241	17.62	9.1E-01	AA806623.1	EST_HUMAN	cb71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
7637	20302	33410	2.34	9.1E-01	U72995.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10075	22723	35940	0.45	9.1E-01	F38432	SWISSPROT	P80-COILIN
12281	25294		27.98	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4346	17085	29714	2.08	9.0E-01	AF09810.1	NT	Homo sapiens neuramin III-alpha gene, partial cds
7291	19974	33052	0.72	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7321	20004		1.18	9.0E-01	D38821.1	NT	Xenopus laevis gene for aldolase, complete cds
9249	21928	35100	0.49	9.0E-01	AF086761.1	NT	Danio rerio semaphorin Z1a mRNA, complete cds
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
5610	18406	31318	2.68	8.9E-01	AF026198.1	NT	Rabbit MHC fragment RLA-DF DNA
6154	18931		1.38	8.9E-01	X60986.1	NT	Oithona nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
8325	21018	34154	0.71	8.9E-01	AF259667.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
11787	24377	37707	2.51	8.9E-01	AE003944.1	NT	Chlamydomonas reinhardtii, section 21 of 94 of the complete genome
12138	24627		2.86	8.9E-01	AE002186.2	NT	Chlamydomonas reinhardtii, section 21 of 94 of the complete genome
12762	26343		2.51	8.9E-01	AI150836.1	EST_HUMAN	q684408.x1 Soares fetal heart_NIH19W Homo sapiens cDNA clone IMAGE:1704879 3'
4505	17240	20873	3.82	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5289	18094	30755	0.67	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10131	22779	35992	0.83	8.8E-01	7658978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11018	23690	36953	4.96	8.8E-01	Z28337.1	NT	Maeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11668	25382		1.8	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1716843
452	13238	25877	1.54	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2401	15122	27859	1.07	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	15644	28286	5.05	8.7E-01	AA595883.1	EST_HUMAN	nn05f1.1 s1 NCL CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
4946	17673		3.17	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5102	17620		0.97	8.7E-01	AJ268085.1	NT	Homo sapiens partial LGALS9 gene for galectin-9, exon 3
7939	20634	33761	0.62	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
8828	21520	34665	0.69	8.7E-01	AD39456.1	EST_HUMAN	qt36606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
8828	21520	34668	0.69	8.7E-01	AD39456.1	EST_HUMAN	qt36606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9638	22290	35483	1.57	8.7E-01	AE004983.1	NT	Pseudomonas aeruginosa PA01, section 524 of the complete genome
10202	22860	36065	0.61	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10202	22860	36068	0.61	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10735	23422	36685	5.25	8.7E-01	BF563970.1	EST_HUMAN	QVO-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11739	24332	37657	5.47	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11739	24332	37658	5.47	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
462	13247		1.76	8.6E-01	X17012.1	NT	Rat IGF1 gene for insulin-like growth factor II
838	19608	26279	3.45	8.6E-01	W69089.1	EST_HUMAN	zd44403.r1 Soares_fetal_heart_Nbt-IH19W Homo sapiens cDNA clone IMAGE:343516 5'
2268	14994	27733	0.96	8.6E-01	4603210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerabrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3608	16361	29003	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3782	16634	29172	1.55	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5808	18597	31524	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5808	18597	31525	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6609	19372	32385	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6609	19372	32386	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7427	20104		0.78	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
7828	20623		1.12	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 121/4
7841	20636	33763	0.55	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9685	22238		0.46	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12518	25144		1.35	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6626	19388	32401	0.95	8.6E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7425	20102	33189	2.51	8.5E-01	BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8317	21010	34147	0.78	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8317	21010	34148	0.78	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8402	21095	34231	0.67	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10248	22898	36105	1.17	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10248	22898	36106	1.17	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12278	25298		2.24	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA
4702	17438	30067	0.73	8.4E-01	AF083976.2	NT	Fowl adenovirus 8, complete genome
5406	25068	30910	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5406	25068	30911	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7708	20372	33485	0.63	8.4E-01	AF051142.1	NT	Manestra brassicae phenolone binding protein 2 precursor (PBP2) mRNA, complete cds
9858	22508		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssii complete genome; segment 5/6
724	13498	26151	2.8	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3091	18858	28497	2.99	8.3E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3780	16542	29177	0.79	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3993	16741	26375	3.35	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5187	17995	30511	2.41	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9588	22221		4.51	8.3E-01	AJ791952.1	EST_HUMAN	hm0112.y5 NCI_OGAP_Cc8 Homo sapiens cDNA clone IMAGE:1078495 5' similar to contains THR.11 THR repetitive element ;
10010	22658	35872	1.27	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10118	22768	35978	3.46	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10572	23287	36505	3.35	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10590	23384		2.03	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11274	23935	37227	2	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2045	14778	27506	2.3	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2083	14815		1.31	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2686	15395		1.06	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
6676	19583	32631	0.76	8.2E-01	AJ010142.1	NT	Amaritia muscaria mRNA for SCIII25 protein
6797	19541	32569	3.49	8.2E-01	AW379493.1	EST_HUMAN	GM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7189	25106	32928	4.74	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8343	21036	34173	0.59	8.2E-01	BE263145.1	EST_HUMAN	6011448892 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
9924	22572	35770	0.65	8.2E-01	AF014530.1	NT	Homo sapiens mRNA for KIAA0030 protein, partial cds
9959	22607	35812	1.37	8.2E-01	AF052659.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
10123	22771	35985	0.59	8.2E-01	AF223988.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22771	35986	0.59	8.2E-01	AF223988.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10283	22831	36145	3.65	8.2E-01	Q8JI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22831	36148	3.65	8.2E-01	Q8JI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11641	24238	37562	4.65	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11735	24328	37652	6.38	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11740	24333	37659	6.02	8.2E-01	H87398.1	EST_HUMAN	yw14002.r1 Soares placenta_8to9weeks_2NbHP8ac9W Homo sapiens cDNA clone IMAGE:252185 5'
12298	24723	31054	2.37	8.2E-01	AJ001261.1	NT	similar to gb:M88072 80S RIBOSOMAL PROTEIN L7A (HUMAN);
2762	15467		1.08	8.1E-01	AF181839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3451	16207	28857	3.08	8.1E-01	AF055068.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3451	16207	28858	3.08	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region
4893	17592		0.74	8.1E-01	AF202634.1	NT	Homo sapiens MHC class 1 region
6223	18997	31973	0.84	8.1E-01	U16790.1	NT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6526	19292	32286	2.66	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6526	19292	32286	2.66	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7229	19814	32887	0.78	8.1E-01	AB007877.1	NT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7412	20089	33173	0.65	8.1E-01	O47477	SWISSPROT	Homo sapiens KIAA0417 mRNA, complete cds
							CYTCHROME B
7811	20508	33628	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (P1cd) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
7811	20508	33629	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (P1cd) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8507	21189	34344	0.83	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8507	21189	34345	0.83	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8668	21360	34507	1.08	8.1E-01	AW242847.1	EST_HUMAN	xr01h03.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW:LYAR_MOUSE
10025	22673	35888	0.7	8.1E-01	P06425	SWISSPROT	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN. ;contains MER22.b1 PTR5, repetitive element;
10311	22858	36174	0.5	8.1E-01	N84541.1	EST_HUMAN	PROBABLE E4 PROTEIN
11464	24067	37374	2.63	8.1E-01	BE938558.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to
11464	24067	37375	2.63	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12022	24550	31110	1.57	8.1E-01	AE001711.1	NT	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
172	12985		3.49	8.0E-01	AJ271510.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
							Staphylococcus aureus partial pta gene for phosphata acetyltransferase allele 15

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
282	13089	25730	13.81	8.0E-01	AJ132772.1	NT	Bos taurus tub and rif genes
1595	14341	27031	1.12	8.0E-01	8394087	NT	Rattus norvegicus protease (prosome, macropain) 28 subunit, alpha (P-sme1), mRNA
2029	14764		1.91	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215091 5'
3076	15841	28484	1.2	8.0E-01	AF127897.1	NT	Salmonella typhimurium diffractory receptor (SBO27) gene, partial cds
3307	16067	28716	1.35	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3680	16443		1.52	8.0E-01	AL162758.2	NT	Nisseria meningitidis serogroup A strain Z2491 complete genome, segment 777
4496	17232	29862	6.05	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
7889	20584		2.25	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-408 NN1012 Homo sapiens cDNA
8423	21116	34254	0.98	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
10878	23556	36803	2.78	8.0E-01	Q92783	SWISSPROT	CREB-BINDING PROTEIN
441	13227	25670	1.16	7.9E-01	D11470.1	NT	Lymnaea disper nuclear polyhedrosis virus gene for DNA polymerase, complete cds
698	13473		1.14	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1600	14346		22.69	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1482 protein, partial cds
1652	14398		1.2	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2259	14986	27726	5.66	7.9E-01	AB004816.1	NT	Oryzobolus curticulus mRNA for mitsugumin29, complete cds
2260	14987	27727	2.4	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3506	16282	28918	3.01	7.9E-01	AF228694.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4288	17008		0.85	7.9E-01	BE263612.1	EST_HUMAN	601182033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4572	17307	29935	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4572	17307	29936	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
6252	19026	32000	0.67	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8008	20703	33831	2.79	7.9E-01	X00996.1	NT	P. sativum GR gene
9447	22124	35304	4.04	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9949	22597	35801	4.47	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
9991	22639	35949	0.91	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10408	23054	36271	1.84	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10516	23162	36389	0.52	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10929	23609		2.74	7.9E-01	7682471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11173	23840	37123	2.02	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
856	13625		2.24	7.8E-01	Z43785.1	EST_HUMAN	HSC1K1041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kb04
2273	14999	27737	7.47	7.8E-01	AW959567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4653	17387	30020	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5978	18760	31724	2.28	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6124	18902	31874	0.88	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6371	19140	32136	0.63	7.8E-01	AL445068.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8389	21082	34216	1.02	7.8E-01	BF106827.1	EST_HUMAN	7154405.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3'
9133	21821	34987	1.3	7.8E-01	Y10159.1	NT	D. discoideum recGAP gene
9231	21910	35083	0.61	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214KD (CAIN) (NUP214), mRNA
10024	22672		0.97	7.8E-01	Q26452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12271	25275		2.5	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-aminocyclopropane carboxylate synthase (ACS5) gene, complete cds
139	12954	25596	7.61	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	13483		2.26	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NC9), butyrophilin-1p
2717	15424	28163	2.21	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3351	16111		0.84	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactoseamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
3586	16340	28985	3.98	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4365	17103	29738	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4365	17103	29739	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31165	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5473	18272	31166	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5866	18653	31594	0.85	7.7E-01	R08600.1	EST_HUMAN	YF24b02.s1 Soares fetal liver spleen 1NF5L Homo sapiens cDNA clone IMAGE:127755 3'
9744	22395	35600	0.51	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhh3, dhh1 and dhh2 genes), complete cds
12161	24944		4.55	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
6008	18789	31751	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6008	18789	31752	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
8425	19193	32189	0.81	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
8751	17920	30555	0.94	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
8751	17920	30585	0.94	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
8951	19433	32449	0.88	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-ketotxin receptor mRNA, complete cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7984	20659	33784	1.38	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HsAR (Hsar) gene, complete cds
8026	20721	33852	1.88	7.6E-01	6857752	NT	Mus musculus edvillin (Advil-pending), mRNA
8026	20721	33853	1.88	7.6E-01	6857752	NT	Mus musculus edvillin (Advil-pending), mRNA
8866	21557	34703	0.74	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9179	21849	35015	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9179	21849	35016	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11330	24021	37325	2.68	7.6E-01	X98347.1	NT	H. aspersa mRNA for neurofilament NF70
11330	24021	37326	2.68	7.6E-01	X98347.1	NT	H. aspersa mRNA for neurofilament NF70
11711	24308		3.64	7.6E-01	AL161582.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11831	24489		3.73	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
500	13284		1.44	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
570	13351	28979	1.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3354	16114	28769	0.95	7.6E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-037E11 5'
7421	20098	33186	1.01	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
11177	23844	37130	1.5	7.5E-01	AB047819.1	NT	Homo sapiens GCMA/GCM1 gene for chorton-specific transcription factor GCMA, complete cds
12228	24682		4.8	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12742	25008	30975	1.46	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328782 (section 29 of 148) of the complete genome
4108	19865	28522	1.78	7.4E-01	AI598146.1	EST_HUMAN	h14509.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2342	15065	27802	0.96	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
4276	17015	28842	4.73	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7743	20439	33562	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7743	20439	33563	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8531	21223	34365	0.83	7.4E-01	BF346268.1	EST_HUMAN	602018456F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154340 5'
8613	21305		0.76	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
8994	21684	34834	6.95	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9054	21743	34901	1.14	7.4E-01	AA187986.1	EST_HUMAN	zp67h01.s1 Strabagene endofthalid cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
10302	22949	36164	0.76	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11665	24260	37682	1.85	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11665	24260	37583	1.85	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11900	24467		3.62	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12008	24542		1.78	7.4E-01	A472641.1	EST_HUMAN	Ia13h01.x1 NCI_OGAP_Lyn5 Homo sapiens cDNA clone IMAGE:2043985 3'
2889	15765	28413	0.8	7.3E-01	P08710	SWISSPROT	HYPOTHETICAL PROTEIN HKLF1 (IRL1) (TRL1)
4575	17310	28938	0.7	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4652	17388	30018	4.37	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5040	17759	30373	1.01	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6511	19278	32276	5.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6511	19278	32277	6.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6994	25103	32735	0.57	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7359	20040	33118	0.66	7.3E-01	Z14193.1	NT	D.melanogaster Cnc mRNA for clathrin heavy chain
7445	20121	33210	7.84	7.3E-01	M28511.1	NT	V.algindyticus sucrose (scfB) gene, complete cds
7445	20121	33211	7.84	7.3E-01	M28511.1	NT	V.algindyticus sucrose (scfB) gene, complete cds
11407	24058	37361	3.83	7.3E-01	AA678019.1	EST_HUMAN	225b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431798 3'
11407	24058	37362	3.83	7.3E-01	AA678019.1	EST_HUMAN	225b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431798 3'
812	13583		3.89	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (aIF-2a) mRNA, complete cds
1850	14685	27398	2.32	7.2E-01	X78140.1	NT	N.tabacum Nelf-4A13 mRNA
2463	15181	27920	1.27	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3063	15829	28473	1.38	7.2E-01	AF168100.1	NT	Fowlpox virus, complete genome
3445	16201	28851	2.56	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-8) gene, vsp417-8/A-1 allele, complete cds
3601	16354	28994	1.06	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
4040	16785		0.7	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
4718	17450	30083	2.65	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5075	17784	30410	0.74	7.2E-01	P33088	SWISSPROT	NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH I)
7112	19800	32854	0.88	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8353	21046	34183	1.11	7.2E-01	AF236081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
8662	21553		0.46	7.2E-01	AV749373.1	EST_HUMAN	AV749373 CB Homo sapiens cDNA clone CBMAFD06 5'
10239	22887	36100	2.33	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
10639	23330	36568	4.02	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
11104	23774	37049	1.27	7.2E-01	S78838.1	NT	Dbs-Dbl guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]

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12422	24798		2.9	7.2E-01	AF000083.1	NT	Aeropyrum pernix genomic DNA, section 67
676	13451	28094	12.73	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3059	15825	28470	11.76	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4184	16925	29555	3.18	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4184	16925	29555	3.18	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
5858	18945	31585	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
5858	18945	31586	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
6850	19550	32580	7.68	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropterin synthase (pr) gene, complete cds
8081	20785	33916	0.58	7.1E-01	H54244.1	EST_HUMAN	y489d09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202861 3'
8635	21327	34469	0.83	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301293-011-409 BT0567 Homo sapiens cDNA
8635	21327	34470	0.83	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301293-011-409 BT0567 Homo sapiens cDNA
9755	22408	35613	1.43	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10309	22956	36172	1.22	7.1E-01	M12961.1	NT	Human T-cell receptor gamma-chain J2 gene
12211	25205		2.21	7.1E-01	AA421492.1	EST_HUMAN	zu06ht11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1207	13958	28624	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1207	13958	28625	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2450	15169	27907	1.13	7.0E-01	N62412.1	EST_HUMAN	y273e07.s1 Soares multiple sclerosis_2NblHMSF Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2450	15169	27908	1.13	7.0E-01	N62412.1	EST_HUMAN	y273e07.s1 Soares multiple sclerosis_2NblHMSF Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
4996	17719		1.78	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21G101
5882	18949		1.11	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8276	20970		11.76	7.0E-01	AE000263.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
8216	21895	35064	0.57	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtd genes, complete cds
8216	21895	35065	0.57	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtd genes, complete cds
10526	23172	36400	0.49	7.0E-01	U34662.1	NT	Danio rerio complement factor B mRNA, complete cds
11064	23734	37008	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11064	23734	37007	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
949	13716	26380	11.02	6.8E-01	U68674.1	NT	Candida albicans equaleone epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds

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949	19715	26391	11.02	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1287	14037	26708	2.74	6.9E-01	AA983530.1	EST_HUMAN	mm28a09.s1 NCI_CGAP_Ges1 Homo sapiens cDNA clone IMAGE:1085176 3'
3213	15976	28627	1.97	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5694	18488	31409	0.91	6.9E-01	AB035982.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
5900	18685	31633	0.82	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6277	19050	32027	1.36	6.9E-01	BE286188.1	EST_HUMAN	60117733F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7697	20360	33474	0.65	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
7879	20574	33700	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7879	20574	33701	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9068	21758		0.79	6.9E-01	AF118048.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9594	22247	35431	0.59	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9594	22247	35432	0.59	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11223	23888	37172	2.38	6.9E-01	D98013.1	NT	Homo sapiens DAN gene, complete cds
11223	23888	37173	2.38	6.9E-01	D98013.1	NT	Homo sapiens DAN gene, complete cds
11878	25197		3.01	6.9E-01	Q99968	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
937	13704	26369	1.05	6.8E-01	AF017784.1	NT	Glerdia intestinalis carbamate kinase gene, complete cds
2680	15389		0.99	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2832	14358	27045	1.49	6.8E-01	AA854475.1	EST_HUMAN	aj76a05.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X58411.1ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4533	17288	28901	1.45	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
9538	22191	35375	1.45	6.8E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11027	23698	36962	1.92	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11027	23699	36963	1.92	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37000	2.4	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11058	23728	37001	2.4	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37527	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37528	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>

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291	13097	25739	44.11	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
330	13131	25766	21.34	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2143	14873	27606	1.73	6.7E-01	AA451864.1	EST_HUMAN	zot12g12.s1 Soares_total_fetus Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2163	15587	27628	2.51	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst45C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2394	15780	28408	3.41	6.7E-01	6676580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4419	17155	29786	0.78	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5422	18221	30832	0.94	6.7E-01	J04836.1	NT	M. barteri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5422	18221	30833	0.94	6.7E-01	J04836.1	NT	M. barteri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6231	19005	31981	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6231	19005	31982	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
7215	19900		4.34	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PAO1, section 167 of 529 of the complete genome
7240	19925	33000	0.92	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10044	22692		0.68	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10873	23553	36800	2.07	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11436	23203	38435	3.59	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11659	24255	37578	1.66	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' and
2505	15222	27984	1.29	6.6E-01	AF076240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2704	16411	28148	1.44	6.6E-01	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3650	18403	28043	4.57	6.6E-01	Y07669.1	NT	C. albicans random DNA marker, 282bp
4089	16832		0.85	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
5125	17843	30461	1.13	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
6240	19014	31988	4.29	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7585	20253	33359	3.76	6.6E-01	AV680508.1	EST_HUMAN	AV680508 GLC Homo sapiens cDNA clone GLCID04 3'
8464	21156	34289	0.52	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9564	22217		2	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12470	24836	31033	1.48	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
610	13398	26019	18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

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610	13388	28020	18.23	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3426	16183	28833	4.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4249	16890	28615	4.23	6.5E-01	AJ272266.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4277	17016	28643	0.78	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5003	17726	30329	2.8	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5357	25087	30843	1.77	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5)
5627	18424	31337	0.62	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6825	19387	32400	1.5	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7566	20236	33340	0.84	6.5E-01	AJ789882.1	EST_HUMAN	wc46802.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321842 3'
9737	22388		0.8	6.5E-01	U78804.1	EST_HUMAN	yt21b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108847 3'
10233	22881	36094	1.96	6.5E-01	AF119876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10529	23228	36460	2.88	6.5E-01	H87583.1	EST_HUMAN	yw17708.r1 Soares_placenta_8to9weeks_2Nbrp8to9W Homo sapiens cDNA clone IMAGE:252516 5'
10595	23280	36518	3.5	6.5E-01	AA601287.1	EST_HUMAN	hu15607.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10690	23381		3.93	6.5E-01	AU139078.1	EST_HUMAN	AU139078 PLAGE1 Homo sapiens cDNA clone PLAGE1007810 5'
11589	24198	37518	2.42	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12267	24710		2.07	6.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12504	25146		1.81	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
245	13054	25694	8.05	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
2593	15307	28043	1.16	6.4E-01	AF161184.1	NT	Pseudomonas fluorescens tryptophan halogenase (pimA) gene, complete cds
3449	16205	28855	2.16	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3842	16593	28230	1.06	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
8510	21202	34347	1.82	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
9889	22637	35848	8.6	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10004	22652	35864	1.22	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12362	24777		5.99	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCC09 5'
425	13211	25858	4.58	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFR-III)
522	13306	25858	2.25	6.3E-01	U3289.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2159	14889	27623	2.02	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigenic resistance locus
2563	15297	28035	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15297	28036	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6873	18765	31716	0.94	6.3E-01	BE083906.1	EST_HUMAN	PM0-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6504	19269	32271	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6504	19269	32272	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8419	21112		3.44	6.3E-01	BE902044.1	EST_HUMAN	601678889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3969351 6'
8784	21476	34824	0.95	6.3E-01	S62927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9120	21808	34975	0.8	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5'
9320	21987	35159	2.45	6.3E-01	9627521	NT	Varicella virus, complete genome
9320	21987	35160	2.45	6.3E-01	9627521	NT	Varicella virus, complete genome
9838	22489		0.67	6.3E-01	AE002328.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10326	22973	36193	1.47	6.3E-01	Z79003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10427	23073	36294	1.19	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10456	23102		0.45	6.3E-01	AW795395.1	EST_HUMAN	PM0-JUM0018-130500-003-g12 UM0018 Homo sapiens cDNA
10693	23667	36924	2.21	6.3E-01	AA877745.1	EST_HUMAN	nr08406.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 O02916 HLARK ;
11308	23967	37268	9.25	6.3E-01	A1904160.1	EST_HUMAN	GM-BT043-090299-046 BT043 Homo sapiens cDNA
11402	24051	37355	1.66	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11681	24180	37495	1.84	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11988	25355	30907	4.37	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12078	24587		1.45	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
12283	25272		2.93	6.3E-01	X83628.1	NT	C.limicola pecD gene
5780	18571	31469	2.31	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7394	20073		3.44	6.2E-01	AF022263.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7443	25114	33209	1.33	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltracin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8200	20894	34031	4.52	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
8755	21447	34595	0.52	6.2E-01	AF034411.1	NT	Lysoresonin oculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9349	20420	33540	1.55	6.2E-01	BE562987.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9410	22072		2.55	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
9978	22626	35834	6.2	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10121	22769	35982	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10121	22769	35983	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10434	23080	36305	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10434	23080	36306	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2393	15114		4.38	6.1E-01	6878076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5449	18248	31137	1.15	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CalMyoD (hlt-1) alternatively spliced genes, complete cds
6770	19514	32540	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6770	19514	32541	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6920	19656	32702	0.84	6.1E-01	AW105853.1	EST_HUMAN	xc50h03.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2567237 3' similar to gb:X12671_mai HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7005	19697	32751	0.72	6.1E-01	Q63768	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8132	20828	33962	3.27	6.1E-01	AF093535.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21386	34528	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21386	34529	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8315	21882	35153	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9315	21982	35154	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9742	22393	35597	0.83	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
8946	22594	35797	1.06	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11738	24331	37655	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11738	24331	37656	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12074	25159	30899	2.28	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
12694	24977		1.57	6.1E-01	X85287.1	NT	M.mazei orfA, orfB, and orfC of archaeal ABC-transporter system
482	13267	25903	1.24	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
548	13331		3.09	6.0E-01	5902899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1341	14089	26765	1.91	6.0E-01	AF066253.1	NT	Human respiratory syncytial virus strain CH-83-53b attachment protein (G) gene, complete cds
3795	16547	29180	0.82	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4165	16905		1.09	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5199	18007	30626	2	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5353	18156	30839	2.86	6.0E-01	AW139713.1	EST_HUMAN	UI-H-B11-eeb-a-10-Q-UI.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6445	19213	32210	2.78	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds

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6563	19328	32335	0.88	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW 136) (CD136 ANTIGEN)
7254	19338	33013	6.99	6.0E-01	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8023	20718	33650	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8023	20718	33651	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9723	22374	35574	1.61	6.0E-01	AB008188.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10173	22821		1.48	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
10980	23684	36921	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperon protein, 419 kD isoform
10980	23684	36922	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperon protein, 419 kD isoform
11540	24140	37449	3.77	6.0E-01	A1420823.1	EST_HUMAN	U0807.x1 NC1_CGAP_P128 Homo sapiens cDNA clone IMAGE2085821 3'
12354	24758	31060	2.25	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12455	24824		2.6	6.0E-01	AA706087.1	EST_HUMAN	Z98905.s1 Soares_fetal_liver_spleen_1NF.L3_S1 Homo sapiens cDNA clone IMAGE462776 3'
12639	25208	30815	3.04	6.0E-01	8055303	NT	Mus musculus cAMP-initiated phosphodiesterase (Pde3a), mRNA
12684	25142		2.06	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-Q30500-016-c03 HT0376 Homo sapiens cDNA
980	13745	28407	1.36	6.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 18 of 183 of the complete genome
3284	16028	28675	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3284	16028	28676	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4196	16937		4.21	5.9E-01	AF162756.1	NT	Rattus norvegicus ceneidin 2 mRNA, partial cds
6373	19142	32139	1.55	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7168	19853	32922	1.32	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7296	19978		0.61	5.9E-01	X68601.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
7898	20593	33725	0.48	5.9E-01	D80911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576563-1718643
8536	21228	34370	0.48	5.9E-01	D12822.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9443	22120	35299	0.82	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KJW31/Cx major outer membrane protein (omp1) gene, complete cds
9813	22464		0.74	5.9E-01	P08463	SWISSPROT	E6 PROTEIN
10088	22738	35951	1.15	5.9E-01	P56284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10569	23264	36502	2.5	5.9E-01	Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10576	23271	36507	1.72	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10881	23561	36808	2.91	5.9E-01	AW837175.1	EST_HUMAN	PM1-DT0041-180100-002-h03 DT0041 Homo sapiens cDNA
11149	23810	37099	1.95	5.9E-01	AF064626.1	NT	Mus spratus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
11458	24062	37368	1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11458	24062	37369	1.58	5.9E-01	P47195	SWISSPROT	JSN1 PROTEIN
12021	24549	31109	2	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12252	24698		4.35	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12465	24832		5.72	5.9E-01	P34928	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1902	14639	27348	1.36	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
2569	16283	28021	1.01	5.8E-01	7306230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4478	17213	28838	4.37	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
5230	18095		0.82	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5444	18243	31131	0.82	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6091	18609	31835	1.09	5.8E-01	D78559.1	EST_HUMAN	HUM500E08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-500E08 5'
6220	18994	31970	0.66	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
6715	18630		2.48	5.8E-01	S65091.1	NT	Cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7787	20482		2.61	5.8E-01	H41571.1	EST_HUMAN	Yn9103.s1 Soares adult brain N265-IB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
7885	20680	33805	0.64	5.8E-01	AJ280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
7885	20680	33808	0.64	5.8E-01	AJ280051.1	EST_HUMAN	qf85410.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8090	20784	33914	3.41	5.8E-01	P14328	SWISSPROT	qf85410.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8090	20784	33915	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8789	21481	34628	8.97	5.8E-01	AJ270774.1	NT	SPORE COAT PROTEIN SP86
8871	21562	34707	0.99	5.8E-01	Q27368	SWISSPROT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8872	21563	34708	0.51	5.8E-01	Q20471	SWISSPROT	TRANSCRIPTION FACTOR E2F
9496	22149		0.81	5.8E-01	BF031608.1	EST_HUMAN	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
10911	23591	36837	7.56	5.8E-01	AJ243213.1	NT	601557774F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827288 5'
10962	23638		3.97	5.8E-01	BF700092.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11089	23769		1.99	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4284403 5'
1490	14227	26912	1.12	5.7E-01	P06727	SWISSPROT	602127577F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4284403 5'
1480	14227	26813	1.12	5.7E-01	P06727	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
3038	15804		0.89	5.7E-01	6755253	NT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
3217	15980	28631	1.62	5.7E-01	Q9WTJ2	SWISSPROT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
						SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVOT1) (MOVOT1)
3495	16251		2.82	5.7E-01	AB033503.1	NT	Populus euramericana pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6282	19036	32011	5.13	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3858590 5'
6811	19374	32388	0.81	5.7E-01	AA194201.1	EST_HUMAN	z338-08.1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:868674 5'
6763	17892	30568	1.33	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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7684	20328	33438	2.14	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
7870	20565		0.5	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tesc4 and Tesc8 genes, alternative transcripts
8279	20973		0.47	5.7E-01	AJ065061.1	EST_HUMAN	HA0895 Human fetal liver cDNA library Homo sapiens cDNA
9689	22350	35544	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9689	22350	35545	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10475	23121	36351	0.72	5.7E-01	BF540982.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068610 5'
11983	24524		1.52	5.7E-01	BE715081.1	EST_HUMAN	MR3-HT0736-180700-003-e02 HT0736 Homo sapiens cDNA
12638	24958		3.01	5.7E-01	BE969722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839783 3'
3357	16117	28772	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3357	16117	28773	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3883	16813	28252	0.97	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4215	16956	28578	0.74	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8702	21394	34641	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCFSP05 5'
8702	21394	34542	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCFSP05 5'
9275	22029	35189	1.08	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11884	24467		2.57	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
							ng75g10.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element:
11897	24535	37272	1.63	5.6E-01	AA493535.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12352	16813	28252	1.69	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12379	24776		2.7	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12773	25027		4.28	5.6E-01	BF573828.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1189	13941	28806	0.85	5.6E-01	8333912	NT	Rattus norvegicus Prothyl Coenzyme A carboxylase, beta polypeptide (Pcob), mRNA
							GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2705	15412	28149	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2705	15412	28150	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2919	15685	28330	1	5.5E-01	5902085	NT	Homo sapiens superkiller viral activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3062	15628		1.55	5.5E-01	H48219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N255-HB55Y Homo sapiens cDNA clone IMAGE:178286 3'
3228	15691	28644	4.22	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3678	16431	29073	1.7	5.5E-01	P49755	SWISSPROT	FOS-RELATED ANTIGEN-1
5082	17801	30419	1.79	5.5E-01	U69097.1	NT	Bos taurus NFkB class II beta-chain BclA-DIB1 gene, partial cds
7187	18873		0.65	5.5E-01	AB015598.1	NT	Carcassius auratus gene for gonadotropin II beta subunit, complete cds
8348	21041	34178	1.04	5.5E-01	AI791786.1	EST_HUMAN	cr82c01.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9687	22319		0.7	5.5E-01	U88415.1	NT	Chinese-Congo hemorrhagic fever virus strain SPV 415/85 nucleoprotein gene, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	22824	36138	0.86	5.5E-01	T05047.1	EST_HUMAN	EST02836 Fetal brain, Stragelene (cat#836206) Homo sapiens cDNA clone HFBCQ35
11087	23757	37033	1.65	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
140	12855	25597	4.81	5.4E-01	7657266	NT	Homo sapiens KIAA0829 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
140	12855	25598	4.91	5.4E-01	7657268	NT	Homo sapiens KIAA0829 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
571	13352	25980	1.16	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
571	13352	25981	1.16	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1248	13997	26864	3.41	5.4E-01	AW89087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2089	14830		3.43	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2552	14980	27719	1.91	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 16,15' beta carotene dioxygenase (beta-diox gene)
5066	17785	30402	0.82	5.4E-01	M74439.1	NT	Rattus rattus UDP glucuronosyltransferase gene, complete cds
5571	18368	31278	0.74	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6068	18876	31845	0.83	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
6028	19884	32710	0.87	5.4E-01	BE966592.2	EST_HUMAN	601860278R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7235	19920	32893	0.81	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7235	19920	32894	0.81	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7237	19922	32897	1.48	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
8890	22540		2.09	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11015	23687	36948	2.87	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11021	24218	37541	3.08	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11021	24218	37542	3.08	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11944	24499		3.5	5.4E-01	A1853398.1	EST_HUMAN	w37g04.x1 NC1_CGAP_UH Homo sapiens cDNA clone IMAGE:2427128 3' similar to gb:M13452 LAMIN A (HUMAN);
503	13287	25921	1.54	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, hepcidin (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2136	14866	27696	1.01	5.3E-01	AF113918.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2136	14866	27697	1.01	5.3E-01	AF113918.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2766	15491	28230	6.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2786	15491	28231	6.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3237	15999	28649	2.74	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSTCL) gene, complete cds
4187	16928		1.58	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5371	18172	30860	1.96	5.3E-01	AI820821.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740711 5'
5371	18172	30861	1.98	5.3E-01	AI820821.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740711 5'
5466	18265	31156	0.84	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5466	18265	31157	0.84	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5559	18358	31268	1.82	5.3E-01	BE945620.1	EST_HUMAN	7a73c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5559	18358	31267	1.82	5.3E-01	BE945620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
8802	21494		1.8	5.3E-01	LO1950.2	NT	7e73d12.x1 NCI CGAP_P228 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
8854	21545	34682	0.81	5.3E-01	BF433956.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
8854	21545	34683	0.81	5.3E-01	BF433956.1	EST_HUMAN	Ronchula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
10111	22759	35971	0.82	5.3E-01	AI954210.1	EST_HUMAN	7q71c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29
11550	24149	37460	7.3	5.3E-01	BE566291.1	EST_HUMAN	repetitive element;
11789	24379	37709	1.72	5.3E-01	Q05783	SWISSPROT	7q71c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29
11877	25206		4.03	5.3E-01	AA916053.1	EST_HUMAN	repetitive element;
797	13568	26229	18.35	5.2E-01	L20770.1	NT	w94b02.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
1141	13898	26557	8.29	5.2E-01	Q9WV30	SWISSPROT	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
1169	13923	26585	1.77	5.2E-01	AF224492.1	NT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
1879	14618		2.35	5.2E-01	AL163285.2	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
2142	14872	27605	2.55	5.2E-01	AB018283.2	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
3117	15882	28521	1.23	5.2E-01	U65942.1	NT	og80e06.s1 NCI CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
3231	15994		1	5.2E-01	D73443.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
3400	16158		1.58	5.2E-01	AL116780.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
3437	16193	28643	2.27	5.2E-01	AA984165.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NFAT5)
							(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
							Homo sapiens phospholipid scramblase 1 gene, complete cds
							Homo sapiens chromosome 21 segment HS21 C085
							Homo sapiens mRNA for KIAA0740 protein, partial cds
							Chlamydomonas abortus strain S28/3 POMPr1A and POMPr80A precursor, genes, complete cds
							Azotobacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
							Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
							am77g05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3023	16376		0.76	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
4568	17303	29930	0.82	5.2E-01	6762947	NT	Mus musculus acetylcholine receptor beta (Acb), mRNA
4953	17679		1.02	5.2E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
5567	18384	31272	0.87	5.2E-01	AA284281.1	EST_HUMAN	zc44d08.T7 Soares_sensocant_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
9630	25126	35474	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9630	25126	35475	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9632	22483	35985	0.48	5.2E-01	AA194518.1	EST_HUMAN	zq05a09.l1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628783 5'
9826	22574	35772	1.35	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12744	25010		7	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
603	13381	26013	1.84	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
633	13412	26047	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
633	13412	26048	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1648	14394		1.09	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
2017	14782		1.29	5.1E-01	BF863036.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
4057	16802	29433	3.86	5.1E-01	A858495.1	EST_HUMAN	W39b12.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427263 3'
4164	16904	29533	2.81	5.1E-01	P86380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5103	17821	30438	1.01	5.1E-01	U72863.1	NT	Human alpha 1a adrenergic receptor (alpha1a) gene, 5' flanking region
6128	18908	31874	0.67	5.1E-01	BE541068.1	EST_HUMAN	601063609F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6183	18950		0.83	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAU07 5'
6818	19479	32502	1.69	5.1E-01	R80873.1	EST_HUMAN	y94e09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8470	21162	34304	0.63	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8470	21162	34305	0.63	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9683	22236	35420	4.33	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9687	22240	35424	3.14	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10060	22708	35928	0.89	5.1E-01	M84579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12086	25137		4.26	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
12928	24745		3.55	5.1E-01	BF439982.1	EST_HUMAN	nac51f10.x1 NCL_CGAP_Birn23 Homo sapiens cDNA clone IMAGE:3408218 3' similar to contains element TAR1 repetitive element;
2130	14861	27590	1.24	5.0E-01	4885562	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2130	14861	27591	1.24	5.0E-01	4885562	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2140	14870	27601	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2140	14870	27602	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3811	16563	29196	1.13	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3854	16604	29241	2.75	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6547	19312		0.65	5.0E-01	BF576199.1	EST_HUMAN	602132842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271839 5'
7562	20232	33334	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7662	20232	33335	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8428	21121		1.82	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8569	21261	34399	0.71	5.0E-01	BF107948.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9368	20429	33547	2.74	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
9625	22178	35362	1.36	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9625	22178	35363	1.36	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10290	22938		1.12	5.0E-01	BE689218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849438 5'
12026	24554		4	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12715	24989		1.86	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12726	24997		4.39	5.0E-01	Q13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
772	13544	26205	2.43	4.9E-01	BF571462.1	EST_HUMAN	602076849F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1656	14402	27090	1.54	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for o-Jun protein, 1978 BP
1898	14638	27345	1.15	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5321	18124	30783	0.89	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
5946	18728	31686	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5946	18728	31687	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7352	20033	33111	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7605	20271	33378	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7605	20271	33379	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
8888	21579		1.45	4.9E-01	BF20791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9086	21775	34939	0.99	4.9E-01	AW338905.1	EST_HUMAN	h80c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807268 3' similar to TR:085714
9186	25431		1.93	4.9E-01	10848863	NT	O95714 HERC2 ;
10216	22884	36076	0.84	4.9E-01	AF063980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10419	23065	36286	0.77	4.9E-01	X80000.1	NT	Mus musculus adenovirus cycle 1 (Adcyl) cDNA, partial cds
11925	24488		1.72	4.9E-01	AF170812.1	NT	H. sapiens DNA for BCL7A gene and BCL7A/GH locus fusion
12708	25392		6.73	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
4288	17037		0.77	4.8E-01	4504850	NT	nc22a11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
							Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5420	18218	30830	10.78	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6579	18342	32356	0.79	4.8E-01	U82882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnnt1) gene, complete cds
6588	19352		3.76	4.8E-01	AA658878.1	EST_HUMAN	mus8f08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7216	19801		1.99	4.8E-01	5031660	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
7565	20235	33339	0.78	4.8E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
7661	20325	33434	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7661	20325	33435	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7805	20500	33621	1.2	4.8E-01	AI820744.1	EST_HUMAN	y77f10.y5 Soares breast 2NblBst Homo sapiens cDNA clone IMAGE:154785 5' similar to contains element
9144	21875		0.92	4.8E-01	BE155148.1	EST_HUMAN	MER8 repetitive element ;
10628	23322		1.88	4.8E-01	X83502.1	NT	PM1-HT0350-201239-004-b04 HT0350 Homo sapiens cDNA
1217	25165		3.04	4.8E-01	AF227565.1	NT	S.cerevisiae ORFs from chromosome X
12795	25216		1.68	4.8E-01	AF132884.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
6422	19180	32186	8.41	4.7E-01	BF217173.1	EST_HUMAN	Chlamydomonas reinhardtii cop gene, exons 1-8
6941	19423	32438	0.94	4.7E-01	AI204374.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7764	20460	33594	0.63	4.7E-01	T11414.1	EST_HUMAN	q72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
7764	20460	33595	0.63	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8874	21684	34816	0.52	4.7E-01	6981501	NT	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
10751	23436		6.11	4.7E-01	AF102673.1	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11022	23694	36957	2.2	4.7E-01	U41089.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
11262	23914	37206	1.61	4.7E-01	BF528658.1	EST_HUMAN	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11349	24039	37342	1.7	4.7E-01	AW889448.1	EST_HUMAN	602043889F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5'
12116	24609		1.52	4.7E-01	BE887763.1	EST_HUMAN	RC8-NT0028-240400-011-E08 NT0028 Homo sapiens cDNA
12237	24689		1.51	4.7E-01	AW341501.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
							hcd1c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809188 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12813	25055		1.63	4.7E-01	AP000007.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position (777)
12817	25300		1.38	4.7E-01	6679502	NT	Mus musculus proteasome (prosome, macropain) 26S subunit, ATPase 3 (Pamc3), mRNA
3728	16479	29116	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3726	16478	29117	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5333	18136	30795	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5333	18136	30796	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5385	18185	30875	3.11	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5385	18185	30876	3.11	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5459	18258	31148	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5472	18271	31163	2.17	4.6E-01	A1247679.1	EST_HUMAN	qt59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5472	18271	31164	2.17	4.6E-01	A1247679.1	EST_HUMAN	qt59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5480	18279	31175	1.8	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5580	18357		0.98	4.6E-01	AF212124.1	NT	Andis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5645	18440		0.77	4.6E-01	BE817247.1	EST_HUMAN	PM0-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
5809	18598	31526	0.99	4.6E-01	D28215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6183	18940	31911	1.21	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6669	19586	32620	3.2	4.6E-01	U62332.1	NT	Emertocella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6669	19586	32621	3.2	4.6E-01	U62332.1	NT	Emertocella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7131	25105	32884	0.57	4.6E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
7629	20295	33403	0.91	4.6E-01	AA483577.1	EST_HUMAN	nt04h05.s1 NCJ_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
7658	20322		0.59	4.6E-01	Q90069	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI)]
8219	20913	34049	10.11	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9201	21870	35035	1.11	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)

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9201	21870	35038	1.11	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9878	22528	35720	1.64	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370788 3'
9878	22528	35721	1.64	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370788 3'
10812	23592		2.3	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10822	23602	36850	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10822	23602	36851	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11450	23217	36449	5.32	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11450	23217	36450	5.32	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12163	24845		1.77	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#61535) Homo sapiens cDNA clone GEN-105F03 5'
1904	14641	27350	1.43	4.5E-01	AE001931.1	NT	Dendrococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1904	14641	27351	1.43	4.5E-01	AE001931.1	NT	Dendrococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2873	15640	28284	4.5	4.5E-01	AA677086.1	EST_HUMAN	z155d02.s1 Soares_fetal_liver_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454178 3'
3312	16072	28722	4.58	4.5E-01	Q05763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3372	16131	28787	1.07	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4007	16753		0.96	4.5E-01	Q26247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4055	16800	29431	0.88	4.5E-01	A1708908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4155	17887		4.25	4.5E-01	AW873495.1	EST_HUMAN	es96s09.x1 Barstead sorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4890	17617	30236	1.1	4.5E-01	BE963445.2	EST_HUMAN	h080g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5461	18260	31151	1.49	4.5E-01	AW608814.1	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:39668023 3'
6510	19275		1.45	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7312	19895	33073	1.27	4.5E-01	M37036.1	NT	COAT PROTEIN
						NT	Rat nuclear proteins B23.1 and B23.2
7609	20180	33273	2.54	4.5E-01	A1858849.1	EST_HUMAN	w32e02.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2428618 3' similar to TR:Q92823 Q92823
7621	20287	33396	0.65	4.5E-01	P50070	SWISSPROT	SW/ISNF COMPLEX 170 KDA SUBUNIT ;
8206	20900		0.86	4.5E-01	M32661.1	NT	DNA PRIMASE
8302	20986	34134	3.5	4.5E-01	A1848596.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
						EST_HUMAN	t256g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282644 3'
							POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8457	21149	34292	0.83	4.5E-01	Q52728	SWISSPROT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
8680	21372		2.34	4.5E-01	11444786	NT	

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8897	21588	34728	0.88	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
8840	22491		1.02	4.5E-01	8630818	NT	Bombayx mori nuclear polyhedrosis virus, complete genome
10392	23038	36254	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HIFBCY17
10392	23038	36255	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HIFBCY17
10772	23455	36898	2.15	4.5E-01	AW581271.1	EST_HUMAN	xc014h01.x1 NCL CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11217	23890		1.52	4.5E-01	AV718382.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1];
11895	25394		3.52	4.5E-01	BE871461.1	EST_HUMAN	AV718382 GLC Homo sapiens cDNA clone GLOCED12 5'
12840	24880		1.88	4.5E-01	BF337531.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12811	24918		3.37	4.5E-01	11422089	NT	602035275F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183280 5'
2388	15109	27847	3.39	4.4E-01	P49765	SWISSPROT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
3310	16070	28719	1.29	4.4E-01	AF058780.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3310	16070	28720	1.29	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3313	16073	28723	2.92	4.4E-01	BF056726.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4209	16950		1.88	4.4E-01	BE378707.1	EST_HUMAN	7891d02.y1 NCL CGAP_B16 Homo sapiens cDNA clone IMAGE:3393795 5'
5334	18137	30797	1.2	4.4E-01	P04829	SWISSPROT	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5334	18137	30798	1.2	4.4E-01	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5602	18397	31309	1.59	4.4E-01	S65019.1	NT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5619	18415	31328	2	4.4E-01	AV720408.1	EST_HUMAN	much [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 360 nt]
5864	18651	31591	1.46	4.4E-01	AI198413.1	EST_HUMAN	q182h11.x1 NCL CGAP_Homo sapiens cDNA clone GLCCSC12 5'
5864	18651	31592	1.48	4.4E-01	AI198413.1	EST_HUMAN	q182h11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861126 3' similar to TR:Q29168 Q29168
6146	18923	31894	1.78	4.4E-01	AW080795.1	EST_HUMAN	UNKNOWN PROTEIN
6236	19010		1.42	4.4E-01	AA776132.1	EST_HUMAN	UNKNOWN PROTEIN
7297	19980	33056	1.04	4.4E-01	AE000571.1	NT	xc27e08.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:Q68154 Q68154
7723	25119		0.6	4.4E-01	AE001188.1	NT	AFLATOXIN B1-ALDEHYDE REDUCTASE;
7740	20436		9.71	4.4E-01	Z11679.1	NT	aa85d41.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
8661	21353	34500	0.84	4.4E-01	AA056427.1	EST_HUMAN	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8049	21738	34896	0.7	4.4E-01	AF112540.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
							Treponema pallidum section 4 of 87 of the complete genome
							S. tuberosum mRNA for induced stolon tip protein (partial)
							z169a03.s1 Stratiogene cdon (#837204) Homo sapiens cDNA clone IMAGE:509838 3'
							HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds

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9082	21771	34934	0.57	4.4E-01	AW612578.1	EST_HUMAN	hm05c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2864222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9180	21860	35025	1.24	4.4E-01	O62838	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
9862	22512	35709	2.18	4.4E-01	A126850.1	EST_HUMAN	gc39f09.x1 NCI_CGAP_Lu16 Homo sapiens cDNA clone IMAGE:1910921 3'
9863	22513		1.88	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
9997	22645	35857	4.31	4.4E-01	P35580	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10273	22921	36132	1.33	4.4E-01	S76404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10273	22921	36133	1.33	4.4E-01	S76404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12148	24635	31095	3.44	4.4E-01		NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12679	24903	31000	3.36	4.4E-01	8627742	NT	Autographa californica nucleopolydnavirus, complete genome
12683	24971		1.91	4.4E-01	P64725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
12786	25152		1.43	4.4E-01	AW363338.1	EST_HUMAN	RC2-CT0320-281199-012-c07 CT0320 Homo sapiens cDNA
402	13187	25835	2.17	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
402	13187	25836	2.17	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
2875	15642		1.64	4.3E-01	AW835289.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3056	15822	28466	0.75	4.3E-01	AW869477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4131	16873	29501	1.29	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4374	13187	25835	1.18	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
4374	13187	25836	1.18	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
4902	17629		1.19	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5280	18085	30742	0.8	4.3E-01	P46634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5280	18085	30743	0.8	4.3E-01	P46634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5788	18589	31515	1.59	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-c08 HT0638 Homo sapiens cDNA
5817	18606	31534	2.02	4.3E-01	AF179825.1	NT	Salmonella enterica serovar typhimurium (SSC186) gene, partial cds
6608	19371	32384	4.78	4.3E-01	AJ001678.1	NT	Columba palumbus japonica ifn-gamma gene
6689	19608	32846	0.6	4.3E-01	AF075629.1	NT	Equus caballus microsatellite 1EX027
6787	19511		0.91	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7328	20011		1.88	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158288 5'
7496	20168	33280	0.61	4.3E-01	U51002.1	NT	Mus musculus Dlx-2 gene, complete cds
8326	21019		2.72	4.3E-01	U67040.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-flaI) genes, complete cds
9154	21885	35053	0.96	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9628	22279	35468	2.18	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
9628	22279	35469	2.18	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10128	22776	35980	0.84	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHOC cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10409	23055	36272	0.5	4.3E-01	H65292.1	EST_HUMAN	TR:O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2 ;
10849	19606	32646	2.45	4.3E-01	AF075629.1	NT	y45b05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208209 3'
11166	23833	37113	1.29	4.3E-01	AW993658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11168	23833	37114	1.29	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
11745	24336	37862	1.84	4.3E-01	AI874332.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
12770	25025		2.18	4.3E-01	AI003022.1	NT	z64d04.x1 NCI CGAP_OV45 Homo sapiens cDNA clone IMAGE:2293351 3'
1337	15566	26761	1.64	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor wihH gene
1941	14676		1.23	4.2E-01	AA761653.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3598	16349	28960	4.4	4.2E-01	AE003947.1	NT	nz24a09.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1286898 3'
3628	16381	28021	1.41	4.2E-01	AI280338.1	EST_HUMAN	Xylella fastidiosa, section 93 of 229 of the complete genome
3698	17886		0.85	4.2E-01	N81203.1	EST_HUMAN	ql94b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878945 3'
3964	16713	28352	0.97	4.2E-01	Q04886	SWISSPROT	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40488
4649	17383	30015	4.88	4.2E-01	AA634068.1	EST_HUMAN	SOX-3 PROTEIN
4731	17463	30100	3.46	4.2E-01	R13467.1	EST_HUMAN	ij59h01.s1 NCI CGAP_P110 Homo sapiens cDNA clone IMAGE:397777 similar to gb:M33800 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
5628	18423	31336	0.82	4.2E-01	BF242055.1	EST_HUMAN	y77e01.t1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'
5693	18497	31408	1.63	4.2E-01	AW854162.1	EST_HUMAN	601878721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
6112	18889	31858	1.01	4.2E-01	AL183247.2	NT	RC3-CT0264-060400-029-g04 CT0264 Homo sapiens cDNA
6852	19552	32582	10.8	4.2E-01	AU159472.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G047
6852	19552	32583	10.8	4.2E-01	AU159472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6911	25101	32694	2.15	4.2E-01	S82504.1	NT	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6993	19686	32734	7	4.2E-01	AL181547.2	NT	Brcal-breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7891	20586	33715	2.21	4.2E-01	AW967448.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7891	20586	33716	2.21	4.2E-01	AW967448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8106	20800	33932	0.61	4.2E-01	4759039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9870	22520		0.94	4.2E-01	AA705007.1	EST_HUMAN	z95f01.at Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10081	22729	35944	0.45	4.2E-01	AF181854.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10993	23039	36266	1.78	4.2E-01	AW863686.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
10972	23648	36901	2.69	4.2E-01	AB023489.1	NT	Oryzias latipes ORG7 mRNA for membrane guanylyl cyclase, complete cds
11370	23977	37277	2.11	4.2E-01	BE960485.2	EST_HUMAN	601603352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
1072	13830	26488	1.83	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210193-142 BT091 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1081	13839	28497	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1081	13839	28498	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2715	15422	28161	1.1	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2841	15708	28355	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2841	15708	28358	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3754	16508	29142	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGG resequences, MAGG Homo sapiens cDNA
3754	16508	29143	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGG resequences, MAGG Homo sapiens cDNA
4241	16982	29607	2.83	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4271	17011		0.82	4.1E-01	AA909257.1	EST_HUMAN	cm33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4618	17353	29888	1.48	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
4868	18057	28708	2.48	4.1E-01	AA906344.1	EST_HUMAN	q94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
5899	18684	31632	4.72	4.1E-01	BF681393.1	EST_HUMAN	602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
7332	20014	33092	2.76	4.1E-01	U67635.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7935	20630	33757	1.38	4.1E-01	BF574804.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
8888	21678	34827	1.39	4.1E-01	6756621	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Stipeepending), mRNA
9465	22075		0.67	4.1E-01	AF160597.1	NT	Volvox gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10163	22811		1.05	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
10310	22957	36173	0.91	4.1E-01	AV649578.1	EST_HUMAN	AV649578 GLC Homo sapiens cDNA clone GLCBVD12 3'
10404	23050	36267	0.61	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10404	23050	36268	0.61	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10478	23124		1.33	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200898-010-c08 HT0137 Homo sapiens cDNA
10743	23430	36673	80.48	4.1E-01	X58700.1	NT	Zea mays ZMIPMS2 gene for 19 kDa zein protein
11366	23177	36404	2	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1)(HBK1)
12475	25360		2.62	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1016	13775	28435	0.82	4.0E-01	8404656	NT	Laqueus rubellus mitochondrialrion, complete genome
1316	14085	28739	0.95	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmation (dmt) mRNA, complete cds
1468	14215		4.05	4.0E-01	6878258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1899	15583	27467	1.16	4.0E-01	Z96933.1	NT	Ascolobolus immersus msc2 gene
1899	15583	27458	1.16	4.0E-01	Z96933.1	NT	Ascolobolus immersus msc2 gene
2166	14886	27619	1.19	4.0E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2166	14886	27620	1.19	4.0E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2808	12952	25595	1.4	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recoguin (Ubr1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2868	16734	28383	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2868	15734	28384	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3683	16436	28080	1.98	4.0E-01	AF088903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3807	16559	29191	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3807	16559	29192	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4767	17499		7.97	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5820	18609	31538	1.23	4.0E-01	AW970810.1	EST_HUMAN	EST382081 IMAGE resequences, MAGK Homo sapiens cDNA
							STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
6345	19115	32104	0.94	4.0E-01	P27285	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7728	20391	33504	0.86	4.0E-01	P27546	SWISSPROT	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7829	20524	33849	0.44	4.0E-01	BF032634.1	EST_HUMAN	Homo sapiens OCTN2 gene, complete cds
7910	20605	33736	1.04	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8904	21595	34736	1.17	4.0E-01	AA323289.1	EST_HUMAN	EST230666 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11560	24159		2.03	4.0E-01	BF030282.1	EST_HUMAN	601558283F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3828092 5'
11721	24315		2.83	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12162	25222		2.26	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12684	24972		2.2	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STES INTERGENIC REGION
1356	14104	26780	1.85	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2648	15358	28101	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2709	15416	28153	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2709	15416	28154	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3083	15858	28499	4.73	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syrB2, cys3 genes and orf3
4059	16804	28435	1.05	3.9E-01	BF562611.1	EST_HUMAN	761d01.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3330169 3'
4832	17660	30270	1.74	3.9E-01	BE728887.1	EST_HUMAN	601563048F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3833699 5'
5843	18631	31566	3.91	3.9E-01	BF208036.1	EST_HUMAN	601962362F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:4082055 5'
7854	20549	33674	0.92	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8760	21452	34600	0.81	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170899-004-508 CT0105 Homo sapiens cDNA
8769	21461		0.86	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCI_CGAP_Br167 Homo sapiens cDNA clone IMAGE:4155322 5'
							xn86d04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821
9134	21822	34988	1.26	3.9E-01	AW195888.1	EST_HUMAN	O94821 KIAA0713 PROTEIN;
							wp76a02.x1 NCI_CGAP_Br125 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR.;
9445	22122	35301	1.46	3.9E-01	AI937337.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9778	22428	36635	3.03	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
9845	22498		0.58	3.9E-01	11465620	NT	Parhydra purpurea mitochondrion, complete genome
10068	22714	35932	0.77	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10722	23410		1.98	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBCQCT11 5'
11763	24344	37674	1.47	3.9E-01	AV702823.1	EST_HUMAN	AV702823 ADB Homo sapiens cDNA clone ADBDBE06 5'
11948	25295		3.37	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12066	24581		2.08	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
12559	24891		1.44	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
156	12971		8.33	3.8E-01	7019488	NT	Homo sapiens protein kinase PKXbeta (pkxbeta), mRNA
1863	14601		1.03	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2460	15178	27918	1.29	3.8E-01	U41846.1	NT	Ceanorhabditis briggsae acetylcholinesterase (ace-1) gene, complete cds
2576	15280	28027	1.62	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2638	15601	28092	3.96	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3003	15769		1.14	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3043	15809	28456	1.39	3.8E-01	AF043383.1	NT	Plautonectes americanus aminopeptidase N (ampN) gene, partial cds
3477	16233	28887	7.98	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3527	16283		0.79	3.8E-01	AB07219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3541	16283		1.22	3.8E-01	AB07219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3739	16492	29127	1.15	3.8E-01	BE164080.1	EST_HUMAN	PIM2-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3897	16947	29287	0.97	3.8E-01	8754095	NT	Mus musculus general transcription factor II (Gtf2), mRNA
4043	16788	29416	0.74	3.8E-01	AJ271361.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5522	18320	31221	1.42	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6247	19021		0.74	3.8E-01	S946825.1	NT	p10n protein (mink, Genomic, 2446 nt)
6528	19294	32298	5.5	3.8E-01	BE072389.1	EST_HUMAN	QV3-BT0537-271289-049-e02 BT0537 Homo sapiens cDNA
6862	19579	32614	4.58	3.8E-01	AJ374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
6840	19502	32527	1.25	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7416	20083		4.42	3.8E-01	X61597.1	NT	Mimulus gene for kalikrein-binding protein
8196	20690	34028	0.86	3.8E-01	M81395.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8455	21147	34289	2.04	3.8E-01	AB048851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8523	21215	34358	1.02	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8716	21408	34651	1.28	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9461	22011		3.55	3.8E-01	T85413.1	EST_HUMAN	ye43h06.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10895	23386		1.87	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11521	24121		3.18	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11693	24298	37610	2.27	3.8E-01	R42550.1	EST_HUMAN	y62h11.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11693	24298	37611	2.27	3.8E-01	R42550.1	EST_HUMAN	y62h11.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12149	24636		4.76	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12270	25316		2.08	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12384	24779		3.39	3.8E-01	BE829256.1	EST_HUMAN	QV3-E10063-190700-271-e05 E10063 Homo sapiens cDNA
12723	24994		1.54	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
12771	25291		1.74	3.8E-01	AF281483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
12788	25040	30868	1.51	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2486	15203	27944	12.24	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3453	16209	28960	9.64	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4204	16945	28572	7.39	3.7E-01	AJ218707.1	EST_HUMAN	ok39cd07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4286	17025	28951	1.3	3.7E-01	AW878037.1	EST_HUMAN	MP3-OT0007-080300-104-R02 OT0007 Homo sapiens cDNA
4357	17085	29730	2.65	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
5678	18470	31386	1.15	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
5860	18647	31588	0.9	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9417	19185	32183	0.66	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6438	19204		0.72	3.7E-01	L10353.1	NT	Mus saxicola hemoglobin mRNA, complete cds
7043	19734	32784	3.23	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7685	20349	33463	0.6	3.7E-01	T68802.1	EST_HUMAN	ye50a07.r3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66324 5'
7719	20383	33497	0.56	3.7E-01	AW511328.1	EST_HUMAN	hd45d05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912457 3' similar to contains Alu repetitive element contains L1.12 L1 repetitive element ;
8227	20921	34059	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8227	20921	34060	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8283	20957	34096	0.65	3.7E-01	AA02812.1	EST_HUMAN	ok43b11.s1 NCI CGAP Le2 Homo sapiens cDNA clone IMAGE:1616701 3'
9101	21789		1.31	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bcdo gene)
10069	22717		0.6	3.7E-01	K00691.1	NT	mouse Ig gamma alpha membrane exons region
10110	22758	35970	4.12	3.7E-01	AJ336411.1	EST_HUMAN	qt46b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
10784	23448	36890	1.98	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
10957	23633	36882	2.81	3.7E-01	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
10957	23633	36883	2.81	3.7E-01	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11443	23210	36441	2.75	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11676	24271	37593	1.43	3.7E-01	D79348.1	EST_HUMAN	HUM230A06B Human aorta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-230A06 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11771	24362		2.87	3.7E-01	6877678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11869	24943		2.11	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12033	24558		3.09	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12488	24847		1.9	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075.5
12548	24886	30895	4.03	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
254	13062	25701	2.17	3.6E-01	AJ009809.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
976	13740		8.22	3.6E-01	U89241.1	NT	Human mbp gene, partial cds
1291	14040	28713	3.83	3.6E-01	T80255.1	EST_HUMAN	y003a05.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443.5
1291	14040	28714	3.83	3.6E-01	T80255.1	EST_HUMAN	y003a05.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443.5
1909	14848	27356	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33702.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419.3
1909	14848	27357	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33702.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419.3
1944	14679	27393	5.7	3.6E-01	AF218207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2047	14780		1.39	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2267	14893		1.05	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2389	15110		2.69	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2479	15197	27836	1.23	3.6E-01	L05436.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2479	15197	27837	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2491	15208	27850	1.43	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181089-011-g07 ST0171 Homo sapiens cDNA
2636	15348	28090	1.44	3.6E-01	P24206	SWISSPROT	PROTEIN L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2900	17884		7.16	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3462	16218	28871	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3462	16218	28872	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4375	17112	28745	1.3	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
4948	17676	30285	2.39	3.6E-01	AW393933.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566.3
5298	18103	30782	0.82	3.6E-01	AJ008583.1	NT	Homo sapiens lipo gene Intron 5
5995	18776	31738	0.85	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6386	19155	32154	1.74	3.6E-01	Y10198.1	NT	Homo sapiens PHOX gene
7048	19739		3.2	3.6E-01	R040300.1	EST_HUMAN	y074a06.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:275987.5
7183	19869	32943	1.9	3.6E-01	AW027174.1	EST_HUMAN	wf72a10.x1 Soares_thymus_NH1Th Homo sapiens cDNA clone IMAGE:2513010.3 similar to TRC015117
8123	20817	33963	0.58	3.6E-01	P88167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1]; SCO-SPONDIN

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	20871	34005	11.45	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8800	21591	34731	2.74	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8900	21591	34732	2.74	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9091	21780	34944	1.17	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9299	21966	35139	1.04	3.6E-01	X17560.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9299	21966	35140	1.04	3.6E-01	X17560.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9369	21844		0.57	3.6E-01	X62825.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
9763	22414	35621	14.67	3.6E-01	Q63194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9893	22543	35735	0.51	3.6E-01	AW752901.1	EST_HUMAN	MF2-CT0222-211089-002-b10 CT0222 Homo sapiens cDNA
9893	22543	35736	0.51	3.6E-01	AW752901.1	EST_HUMAN	MF2-CT0222-211089-002-b10 CT0222 Homo sapiens cDNA
10864	23544	36791	3.31	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3868697 5'
11062	23722	36993	4.12	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
							Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11421	23188	38419	3.4	3.6E-01	AE000856.1	NT	Homo sapiens Hlb5 gene for hair keratin, exons 1 to 9
11903	25415		1.83	3.6E-01	Y19210.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
11978	24522		1.4	3.6E-01	D80901.1	NT	Escherichia coli K-12 MG1655 section 226 of 400 of the complete genome
11987	24528		3.89	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 226 of 400 of the complete genome
12135	24624		4	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12493	24630		2.12	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12746	25363		2.23	3.6E-01	AW190229.1	EST_HUMAN	x60e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879116 3' similar to gblK00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
204	13017	25657	2.05	3.5E-01	6878933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
708	13482	26131	1.59	3.5E-01	7708136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	13482	26132	1.59	3.5E-01	7708136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
762	13535	26194	4.25	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1615	14362	27053	1.1	3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1636	14362	27069	1.96	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15008	27747	1.35	3.5E-01	P06788	SWISSPROT	HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2612	15900	28066	1.76	3.5E-01	AA223252.1	EST_HUMAN	z08a09.s1 Striatogene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16537		0.85	3.5E-01	AA642138.1	EST_HUMAN	nr60403 at NCJ_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4231	16972	29586	1.67	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds
4443	17179	29805	0.94	3.5E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181089-011-g02 HT0218 Homo sapiens cDNA
4627	17362	29895	1.02	3.5E-01	Y18477.1	NT	Mus musculus Alox12b gene 5' flanking region
4880	17607	30230	4.58	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
5251	18057	30885	0.76	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5251	18057	30886	0.76	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5462	18261	31152	1.13	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6143	18921		0.98	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA
6314	19085	32070	0.6	3.5E-01	AA431833.1	EST_HUMAN	zw79103.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782428 5' similar to TR:G1066835
6359	19129	32124	0.68	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6566	19331	32338	1.08	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
6856	19498		4.24	3.5E-01	X96505.1	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
7441	20118	33207	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7441	20118	33208	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7970	20865		2.19	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7973	20868	33780	0.71	3.5E-01	BF358871.1	EST_HUMAN	RC4-E10024-260600-014-c07 E10024 Homo sapiens cDNA
8368	21059		0.63	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
8825	21517	34682	1.17	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9636	22288	35481	1.62	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9786	22437	35644	5.64	3.5E-01	226825.1	NT	Xlaevis gene for albumin including HP1 enhancer
9887	22517	35713	0.96	3.5E-01	BE174784.1	EST_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10635	23327	36584	2.78	3.5E-01	X61084.1	NT	C.griseus rhodopsin gene for opsin protein
10949	23625	36875	2.39	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
10949	23625	36876	2.39	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11505	24106	37419	1.34	3.5E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11595	24184	37499	1.64	3.5E-01	N77597.1	EST_HUMAN	yz90h12.1 Soares_multiple_sclerosis_2NblHMSIP Homo sapiens cDNA clone IMAGE:280375 5'
11618	24216		1.71	3.5E-01	M62865.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11694	24279	37601	1.51	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
11776	24367		1.36	3.5E-01	A084773.1	EST_HUMAN	HA0542 Human fetal liver cDNA library Homo sapiens cDNA
12063	24578		1.47	3.5E-01	X64565.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12214	24676		2.32	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12402	24787		1.4	3.5E-01	AE001691.1	NT	Thermotoga maritima section 3 of 138 of the complete genome
12783	25288	30723	3.33	3.5E-01	H80814.1	EST_HUMAN	ys84f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
12783	25289	30724	3.33	3.5E-01	H80814.1	EST_HUMAN	ys84f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	13466		1.85	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
955	13720	26386	7.61	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
1303	14052	28725	1.72	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2400	15121	27858	2.62	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3001	15767	28415	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3001	15767	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3146	15910	28555	1.08	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3159	15922	28568	6.23	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNCGC1) mRNA, complete cds
3338	16098	28749	0.9	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3522	16278	28933	3.48	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3770	16522		1.09	3.4E-01	BF448010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR-Q8UJ15
4029	16774		2.38	3.4E-01	AA584186.1	EST_HUMAN	Q8UJ15 DJ18C8.1
4460	17196	29823	0.82	3.4E-01	AF168341.1	NT	h011b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4589	17334	28983	1.54	3.4E-01	BE068912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4698	17625		3.23	3.4E-01	AI240873.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5143	17862		0.98	3.4E-01	U79746.1	NT	q95c05.x1 NCI_CGAP_K163 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5599	18394	31304	2.82	3.4E-01	AL161594.2	NT	Homo sapiens serotonin transporter (SERT) gene, promoter region, exons 1B and 2, and partial cds
5721	18613		6.09	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5917	18702		1.09	3.4E-01	L02871.1	NT	zn12a11.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
5940	18722	31681	0.89	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6017	18798	31759	2.43	3.4E-01	AW204505.1	EST_HUMAN	60157181T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6141	18919	31889	1.81	3.4E-01	AL120544.1	EST_HUMAN	ULH-B11-est-e-12-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6944	19406		1.66	3.4E-01	N96225.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
							zb53e12.s1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:307342 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6848	19548	32578	1.02	3.4E-01	A468082.1	EST_HUMAN	hm3g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
6859	19441	32456	0.59	3.4E-01	BF678702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
7806	20601		0.49	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8135	20829	33984	0.6	3.4E-01	Y14930.1	NT	Homo sapiens TGRAV28 gene, allele A4, partial
8188	20882		0.47	3.4E-01	BF449010.1	EST_HUMAN	7n84a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8LU16 Q8LU16 DJ1808.1;
8388	21079		1.51	3.4E-01	AA337083.1	EST_HUMAN	EST41705 Endometrial tumor Homo sapiens cDNA 5' and
8461	21153	34298	0.72	3.4E-01	L04680.1	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
8751	21443	34500	1.7	3.4E-01	Q83382.4	NT	Bovine enterovirus strain K2577, complete genome
9112	21800	34864	4.42	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9112	21800	34865	4.42	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9321	21888		0.51	3.4E-01	AB017510.1	NT	Ephydratia furvialis mRNA for PLC-gammaS, complete cds
9346	20417	33536	4.67	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9348	20417	33537	4.67	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9397	22059	35229	0.5	3.4E-01	AF183957.1	NT	Dichostelium discoideum putative CMF receptor CMFR1 mRNA, complete cds
9695	22248	35433	1.01	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scsf-1) mRNA, complete cds
9789	22440	35648	1.88	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10376	23022		0.62	3.4E-01	AE004098.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10940	23620		4.72	3.4E-01	AE000981.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
10984	23659	36812	2.6	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11032	23703	36971	2.17	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11253	23915	37207	1.61	3.4E-01	M28856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11253	23916	37208	1.61	3.4E-01	M28856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11483	24084	37398	1.88	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-gliadinMUC18, complete cds
11513	24113	37423	3.65	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11786	24378	37706	1.72	3.4E-01	BF061948.1	EST_HUMAN	7n89412.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3480846 3'
11861	24445	37786	1.58	3.4E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11881	24455		1.85	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12197	24686		11.43	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12224	25192		1.61	3.4E-01	BE218652.1	EST_HUMAN	hm42f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13 PTR5 repetitive element;

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12280	25292		2.28	3.4E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12391	24781	31036	2.2	3.4E-01	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
12688	24974		1.82	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes.>
13	12840	25453	10.77	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
103	12840	25453	4.4	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
435	13221	25967	0.9	3.3E-01	AL161845.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
618	13397	26032	2.01	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1178	13931	26597	2.85	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1284	14034	26705	3.76	3.3E-01	BF568880.1	EST_HUMAN	602184018T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300281 3'
1336	14085	26760	1.2	3.3E-01	U43626.1	NT	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
1601	14947	27036	1.47	3.3E-01	6756685	NT	Mus musculus discitgrin 5 (Dign5), mRNA
1731	14473		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST136722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2022	14757		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath cultar membrane protein MopB (mopB) gene, complete cds
2404	15125		4.62	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (uridine phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2949	15715	28368	1.87	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3051	15917	28462	1.48	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3486	16243	28999	1.07	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L-1 gene, complete cds
3789	16541	29178	2.1	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3789	16551	29183	0.97	3.3E-01	P22802	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3932	16682	29323	1.03	3.3E-01	4757739	NT	Homo sapiens A kinase (PRKA) anchor protein 5 (AKAP5), mRNA
3947	16697	29336	1.47	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3983	16731	29365	1.79	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4334	17073		1.6	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4841	17375		1.23	3.3E-01	AI539114.1	EST_HUMAN	tp78612x1 NCL CGAP_U8 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gp-X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4786	17517	30739	1.22	3.3E-01	D64003.1	NT	Synochocystis sp. PCC6803 complete genome, 22/27, 2755703-2868768
5146	17865		0.96	3.3E-01	AW937982.1	EST_HUMAN	QV0-DT0047-170200-123-108 DT0047 Homo sapiens cDNA
5241	18047	30675	2.61	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5241	18047	30676	2.61	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5700	18494	31417	0.74	3.3E-01	BF213973.1	EST_HUMAN	60184800F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
5856	18643	31882	1.8	3.3E-01	BE619630.1	EST_HUMAN	601472768T1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3875753 3'
5858	18843	31583	1.9	3.3E-01	BE619660.1	EST_HUMAN	601472768T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
5847	18729	31888	1.18	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6695	18612	32651	0.71	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6695	18612	32652	0.71	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6789	19533	32560	4.82	3.3E-01	AI628131.1	EST_HUMAN	ly84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
6789	19533	32561	4.82	3.3E-01	AI628131.1	EST_HUMAN	ly84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7682	20346	33458	1.68	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8460	21152	34286	18.62	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
8659	21351	34497	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8659	21351	34498	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9012	21702	34852	0.81	3.3E-01	Q62825	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEK 1)
9278	22032	35203	0.81	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9278	22032	35204	0.81	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9411	22073	35244	2.62	3.3E-01	N69866.1	EST_HUMAN	z667h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287849 3'
9452	22002	35174	2.77	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9891	22541		2.27	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10622	23315	36554	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10622	23315	36555	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10951	23628		1.7	3.3E-01	BF528499.1	EST_HUMAN	602070802F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213585 5'
11198	23861	37147	11.61	3.3E-01	BE218351.1	EST_HUMAN	h51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11317	24008	37313	3.23	3.3E-01	P47863	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (LECTIN LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-28) (CBP30)
11719	24313		3.08	3.3E-01	A808621.1	EST_HUMAN	ab71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11741	12840	25453	1.87	3.3E-01	X070690.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
11977	24521	37268	1.71	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12876	24967		3.34	3.3E-01	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
444	13230		2.33	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
701	13476		1.43	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1139	13894	26555	27.53	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1259	14008	26677	1.36	3.2E-01	Z50202.1	NT	P. vulgaris arcs-1 gene
1369	14117	26792	5.42	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1767	14509	27210	1.25	3.2E-01	Z36041.1	NT	
1777	14519	27222	4.7	3.2E-01	AW957194.1	EST_HUMAN	S.cerevisiae chromosome II reading frame ORF YBR172c
1777	14519	27223	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST368264 MAGE resequences, MAGD Homo sapiens cDNA
1835	14574	27266	1.23	3.2E-01	AL111695.1	NT	EST368264 MAGE resequences, MAGD Homo sapiens cDNA
2157	14897	27621	2.52	3.2E-01	BF203817.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2543	15257		2.01	3.2E-01	7710079	NT	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:411512 5'
2713	15420	28159	1.08	3.2E-01	AF06568.1	NT	Mus musculus Pbx/Notch1 1 homeobox (Pbxo1), mRNA
3594	16347		0.77	3.2E-01	D10872.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
4305	17044	28669	0.91	3.2E-01	4759195	NT	Humam h NAT allele 3-2 gene for arylamine N-acetyltransferase
4363	17101	29736	1.52	3.2E-01	M18818.1	NT	Homo sapiens symplekin (SYM) mRNA
4484	17200	29826	1.21	3.2E-01	Q10288	SWISSPROT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4688	17422		6.7	3.2E-01	BF683817.1	EST_HUMAN	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4826	17557	30179	1.17	3.2E-01	Q67081	SWISSPROT	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4965	17690	30299	0.74	3.2E-01	BE782748.1	EST_HUMAN	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3)(ACCESSORY ADHESIN PROTEIN 3)(P69)
5190	17998	30621	3.26	3.2E-01	BE173984.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868799 5'
5868	18655	31508	1.07	3.2E-01	L27221.1	NT	CMD-H170569-060300-269-f10 HT0569 Homo sapiens cDNA
6211	18986	31963	0.9	3.2E-01	AF016494.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6501	19266	32288	0.64	3.2E-01	AV718037.1	EST_HUMAN	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c
6634	19396		1.09	3.2E-01	AB002359.1	NT	AV718037 FH7A Homo sapiens cDNA clone FH7AABH01 5'
7755	20451	33575	0.51	3.2E-01	AJ277661.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8072	20766	33695	1.48	3.2E-01	M60266.1	NT	Homo sapiens perfl LMO1 gene for LIM domain only 1 protein, exon 1
8164	20858	33990	0.45	3.2E-01	AJ231001.1	NT	Rat ISO-alpha natriuretic factor gene, complete cds
8265	20959	34098	14.41	3.2E-01	X02508.1	NT	Rattus norvegicus repeat, map NOS-D12W.ox1
8268	20962	34103	13.76	3.2E-01	BF311635.1	EST_HUMAN	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8361	21054		1.38	3.2E-01	AL161574.2	NT	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8398	21091	34228	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076627 5'
8398	21091	34227	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076627 5'
8471	21163	34306	2.65	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 228 of the complete chromosome 1
8571	21263	34401	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8571	21263	34402	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8665	21656	34807	0.51	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8976	21668		2.18	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9048	21737	34894	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9048	21737	34895	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9894	22544	35737	3.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, rpoC and rpoD genes, complete cds; and unknown genes
10099	22747	35662	0.45	3.2E-01	BE326230.1	EST_HUMAN	h98f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10210	22858		3.41	3.2E-01	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
10566	23261	36498	3.94	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HFB0221
12010	25317		3.91	3.2E-01	U07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12392	26374		1.44	3.2E-01	BE868948.1	EST_HUMAN	601507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909532 5'
12524	24871		4.21	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12655	24955		2.07	3.2E-01	U39874.1	NT	Homo sapiens diacylglycerol deaminase gene, complete cds
12712	25354	30606	1.76	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2677	15386	28128	2.89	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2702	15532	28145	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2702	15532	28146	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2862	15630		1.29	3.1E-01	AW628036.1	EST_HUMAN	h94h08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3170	15633		3.35	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KIAMRE, exon 6
3887	16637	28276	0.8	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4908	17638	30250	0.73	3.1E-01	AE003684.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5390	18190	30882	0.73	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5513	18311	31212	0.73	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HI1238
5514	18312	31213	0.67	3.1E-01	Z74889.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141w
5524	18322		0.88	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5685	18478	31396	2.11	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6191	25087	31942	0.59	3.1E-01	R94322.1	EST_HUMAN	yc41f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198367 5'

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Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6374	19143	32140	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-504 HN0001 Homo sapiens cDNA
6439	19207	32203	1.01	3.1E-01	AI264458.1	EST_HUMAN	q39d01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
6563	19346	32360	3.91	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6873	25061	30545	2.41	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7579	20248	33354	0.77	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8546	21238	34381	1.71	3.1E-01	IR45318.1	EST_HUMAN	Yg48f01.s1 Soares Infant brain T1N1B Homo sapiens cDNA clone IMAGE:35639 3'
9802	22463	35666	0.64	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
9867	22615	35818	1.05	3.1E-01	BF69839.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
9867	22615	35819	1.05	3.1E-01	BF69839.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10029	22677	35893	1.74	3.1E-01	AI244001.1	EST_HUMAN	qj61e11.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:4095814 5'
10201	22849		0.63	3.1E-01	T56325.1	EST_HUMAN	HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10741	23428	36672	1.28	3.1E-01	BF216117.1	EST_HUMAN	y647h08.s1 Strategene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M01036_m22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11524	24124	37430	2.56	3.1E-01	7662291	NT	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
12133	24623		1.48	3.1E-01	AF294308.1	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12185	24647		3.03	3.1E-01	AF304162.1	NT	Anolis opalinus isolet Q5 NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12304	24728		2.62	3.1E-01	AF196953.1	NT	Silvestrodon vitreum 40S ribosomal protein S11 mRNA, partial cds
12680	24960		3.46	3.1E-01	AF196778.1	NT	Homo sapiens membrane-bound aminopeptidase P (ANPEP2) gene, complete cds
12699	25347		1.35	3.1E-01	10946623	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
247	13056	25698	14.52	3.0E-01	AJ271735.1	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrpl-pending), mRNA
1202	13954	26618	2.51	3.0E-01	AW300400.1	EST_HUMAN	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
1497	14244	26830	6.57	3.0E-01	AJ006795.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2132	14862	27592	1.2	3.0E-01	AF237778.1	NT	xs63f08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
3206	15969		1.18	3.0E-01	AB030481.1	NT	Balaenoptera physalus gene encoding arial natruretic peptide
3946	16597	28234	1.46	3.0E-01	AW917785.1	EST_HUMAN	Rattus norvegicus Ca ²⁺ /calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
4477	17212	29837	1.95	3.0E-01	AJ008765.1	NT	Corynebacterium sp. ALY-1 alyP gene for polyglutamate lyase, complete cds
5267	18073	30702	7.22	3.0E-01	BE741629.1	EST_HUMAN	PM1-STU262-261189-001-g01 ST0262 Homo sapiens cDNA
5349	18152	30833	0.77	3.0E-01	AF226247.1	NT	Balaenoptera physalus gene encoding arial natruretic peptide
							601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
							Cantagallo orthopoxvirus hemagglutinin gene, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5417	18216	30824	3.94	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5417	18216	30825	3.94	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5453	18252	31142	4.77	3.0E-01	U01247.1	NT	Mus musculus 120/ev Clara cell 10 kd protein (mCC10) gene, complete cds
6732	18566	32598	3.06	3.0E-01	D16313.1	NT	Mouse cyclotaxin 15 gene, complete cds
6762	17831	30567	0.61	3.0E-01	U02398.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
6827	19488	32510	0.85	3.0E-01	AF228247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
7021	19713	32770	0.71	3.0E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
7227	19912	32985	2.77	3.0E-01	10947007	NT	Mus musculus midnclin (Mdn-pending), mRNA
7400	20078	33159	1.37	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7827	20522	33648	1.3	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8271	20985		2.97	3.0E-01	6910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f), mRNA
8374	21067	34207	1.32	3.0E-01	BE566083.1	EST_HUMAN	601338079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8728	21420	34584	0.51	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbC) gene, partial cds
8770	21462		0.8	3.0E-01	7661685	NT	Homo sapiens DKFZP566M0122 protein (DKFZP566M0122), mRNA
9118	21806	34972	0.81	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative
9856	22506		43.84	3.0E-01	BE001129.1	EST_HUMAN	arthritis-like phosphoribosyltransferase gene, partial cds; and unknown gene
9868	22518	35714	1.25	3.0E-01	BF574612.1	EST_HUMAN	RC2-BN0074-240400-110-112 BN0074 Homo sapiens cDNA
10042	22690	35608	0.49	3.0E-01	AF152598.3	NT	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4286336 5'
10042	22690						Actinobacillus actinomycetomycetans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE),
10042	22690	35909	0.49	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetomycetans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE),
10294	22841	36155	0.84	3.0E-01	AW118111.1	EST_HUMAN	TadF (tadF), and TadG (tadG) genes, complete cds
10296	22843	36157	1.88	3.0E-01	AB030231.1	NT	xe03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10316	22863	36179	0.73	3.0E-01	BF683841.1	EST_HUMAN	Aspergillus oryzae btpA gene for ER chaperone BIP, complete cds
10316	22863	36180	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
11772	24363	37694	1.95	3.0E-01	H51026.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
11772	24363	37695	1.95	3.0E-01	H51026.1	EST_HUMAN	yp84b10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12416	25302		2.52	3.0E-01	AJ297631.1	NT	yp84b10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12693	25345		5.51	3.0E-01	6877766	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
2018	14753	27481	1.43	2.9E-01	AE000736.1	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
2245	14973	27710	1.16	2.9E-01	AF222718.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
3248	16808	28658	2.73	2.9E-01	AW754239.1	EST_HUMAN	Chrysodidymus synnoides mitochondrion, complete genome

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3246	16008	28659	2.73	2.8E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-f12 CT0328 Homo sapiens cDNA
3877	16627	29285	0.72	2.8E-01	A1610838.1	EST_HUMAN	tp21a11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4052	16797	29427	0.73	2.8E-01	AB016428.1	NT	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4084	16808		0.77	2.8E-01	AW002802.1	EST_HUMAN	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4462	17188	28813	1.1	2.8E-01	AA284468.1	EST_HUMAN	wr02110.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
5177	17988		1.68	2.8E-01	R37485.1	EST_HUMAN	zs57d12.r1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
5310	18507	32532	0.79	2.8E-01	AF321001.1	NT	yf77e12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28281 3'
5677	18471	31387	5.19	2.8E-01	X58098.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5677	18471	31388	5.19	2.8E-01	X58098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5689	18482	31401	6.4	2.8E-01	8679862	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5685	18747	31708	1.47	2.8E-01	AA418145.1	EST_HUMAN	Mus musculus Eph receptor A8 (EphA8), mRNA
6187	18984	31937	1.08	2.8E-01	A1797128.1	EST_HUMAN	z397b12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6233	19007	31984	2.4	2.8E-01	U03420.1	NT	wet2c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.t1 L1 repetitive element;
6365	19135	32130	0.58	2.8E-01	R69194.1	EST_HUMAN	Bos taurus myosin I mRNA, complete cds
6365	19135	32131	0.58	2.8E-01	R69194.1	EST_HUMAN	y39408.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141815 5'
6621	19383		0.58	2.8E-01	Z50158.1	NT	y39408.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141815 5'
6680	17968	30523	1.52	2.8E-01	AF142328.1	NT	D.discoideum gene for 34 kD actin binding protein
6996	19688	32737	2.95	2.8E-01	Q04399	SWISSPROT	Mus musculus Flii protein (Flii) gene, complete cds; and Lgln protein (Lgln) gene, partial cds
7059	19750	32813	2.08	2.8E-01	AF100956.1	NT	PUTATIVE MULTICOPPER OXIDASE YDR508C
7820	20515	33640	1.67	2.8E-01	BE540422.1	EST_HUMAN	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
7820	20515	33641	1.67	2.8E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8049	20743	33875	0.48	2.8E-01	AJ237937.1	NT	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8049	20743	33876	0.48	2.8E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8062	20756		0.94	2.8E-01	BF217743.1	EST_HUMAN	Bos taurus partial stat5A gene, exons 5-19
8237	20831		0.49	2.8E-01	AF197456.1	NT	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
							Buchnera aphidicola plasmid pLeu isolates M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8493	21185	34328	0.84	2.8E-01	AU160910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8823	21515	34680	1.02	2.8E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
8931	21622	34765	0.65	2.8E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9145	21878	35040	0.78	2.8E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
9145	21878	35041	0.78	2.8E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
10810	23493	36728	1.93	2.8E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11114	23784	37059	1.75	2.8E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11114	23784	37060	1.75	2.8E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11575	24174	37489	1.59	2.8E-01	AA835373.1	EST_HUMAN	ng3ch02.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
11579	24178	37493	3.55	2.8E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
11600	24189	37519	1.62	2.8E-01	U3025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11600	24189	37520	1.62	2.8E-01	U3025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12452	24821	31024	4.05	2.8E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12741	25007	30973	1.88	2.8E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12741	25007	30974	1.88	2.8E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
555	13338		1.7	2.8E-01	U87138.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
580	13342		1.01	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1061	13819	28481	3.69	2.8E-01	AF168050.1	NT	Gulra guira oocyte maturation factor Mos (o-mos) gene, partial cds
1264	14003	28671	1.62	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1254	14003	28672	1.62	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1268	14017	28684	1.34	2.8E-01	D85550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1651	14397	27087	1.11	2.8E-01	AF076238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
1720	14463	27163	2.04	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0384-120200-065-505 CT0384 Homo sapiens cDNA
2006	14742	27467	2.35	2.8E-01	AL047620.1	EST_HUMAN	DKFZp58612321_j1 586 (synonym: huler) Homo sapiens cDNA clone DKFZp58612321
2127	14858	27588	1.41	2.8E-01	AW511195.1	EST_HUMAN	h444803.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2475	15183	27833	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2475	15183	27834	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2549	15284		1.89	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2670	15380	28118	0.87	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2970	15736		1.29	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2971	15737	28388	2.04	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
2971	15737	28387	2.04	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3373	16132	28788	1.13	2.8E-01	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-694000 nt. position (4/7)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3978	16728	29360	1.59	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4174	16914		1.95	2.8E-01	AI090888.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
4422	17158	29789	0.99	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4427	17163	29793	2.31	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4772	17504	30126	1.19	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polypeptide precursor, gene, partial cds
4777	17508	30131	2.67	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4808	17539	30162	1.23	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5'
4829	17560	30182	1.91	2.8E-01	AI272669.1	EST_HUMAN	q150c11.x1 Soares_Nht-IMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element/contains element LTR5 repetitive element ;
5228	25064	30660	24.65	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5519	18317	31218	3.07	2.8E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
5727	18519		0.95	2.8E-01	AW992683.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
5848	18635		0.63	2.8E-01	AA404576.1	EST_HUMAN	Z41101.r1 Soares ovary tumor NhtOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6083	25418		0.65	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6123	18901	31869	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6123	18901	31870	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6632	19394	32409	8.34	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B14-9d4-04-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7341	20022		1.17	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7382	20062	33140	0.68	2.8E-01	X69680.1	NT	L. esculentum ypt2 mRNA for GTP-binding protein
7691	20686	33811	1.28	2.8E-01	AI346128.1	EST_HUMAN	qp48h01.x1 NCL CGAP_Oc8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
7981	20686	33812	1.28	2.8E-01	AI346128.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8108	20802	33935	1.92	2.8E-01	U51688.1	NT	qp48h01.x1 NCL CGAP_Oc8 Homo sapiens cDNA clone IMAGE:1926288 3' similar to gb:X06323_cds1
8412	21105	34244	0.61	2.8E-01	AA911629.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8488	21180		7.34	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5'
9366	21941	35115	0.92	2.8E-01	U17251.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9611	22264		0.88	2.8E-01	L13654.1	NT	602022987F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158525 5'
9788	22439	35646	0.66	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scot-2) gene, complete cds
							Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
							Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9788	22439	35847	0.68	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9850	22500	35700	0.52	2.8E-01	AF284383.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
9880	22608	35813	3.35	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10211	22859		1.47	2.8E-01	8626154	NT	Fujinami sarcoma virus, complete genome
10251	22889	36109	0.8	2.8E-01	BE698727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839765 3'
10844	23335	36573	2.42	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
10844	23335	36574	2.42	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
10871	23362	36603	3.83	2.8E-01	BF685970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078028 5'
10784	23477	36719	1.33	2.8E-01	AF051682.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11247	23909		4.51	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
11593	24162	37510	17.65	2.8E-01	AL138074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
12408	24789		15.41	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12509	24861	31013	4.22	2.8E-01	BE178899.1	EST_HUMAN	PMA-HT0608-030400-001-607 HT0608 Homo sapiens cDNA
12632	24877	31018	1.77	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955698 5'
12685	25306		2.52	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
12808	25401		1.49	2.8E-01	AW025400.1	EST_HUMAN	wu86g05.x1 NCI CGAP_Ku83 Homo sapiens cDNA clone IMAGE:2527828 3'
464	13249	26890	3.97	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
589	13377	26907	3.25	2.7E-01	AA450061.1	EST_HUMAN	z338b10.s1 Soares_tet1_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1238	13887	26854	2.13	2.7E-01	AB004608.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1617	14984		1.58	2.7E-01	X78815.1	NT	Glembia SR2 gene
1722	14465	27164	3.5	2.7E-01	W58067.1	EST_HUMAN	z022h10.l1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1789	14511	27212	2.56	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2131	15586		2.25	2.7E-01	AF047576.1	NT	Rattus norvegicus vesicular monocamine transporter type 2, promoter region and exon 1
2367	15089	27826	10.01	2.7E-01	Y13888.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial
2457	15175	27914	4.07	2.7E-01	A1310858.1	EST_HUMAN	tx49c11.x2 NCI CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
2898	15666	28314	1.2	2.7E-01	AF251276.1	NT	Mus musculus sarfin protease inhibitor 14 (Spi14) mRNA, complete cds
2883	15749		2.53	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060800-385-605 HT0875 Homo sapiens cDNA
3283	16044	28693	0.68	2.7E-01	8393920	NT	Rattus norvegicus insulin receptor (Insr), mRNA
3992	16740	28374	1.97	2.7E-01	A1928015.1	EST_HUMAN	w82e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4002	16749	29380	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4002	16749	29381	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4008	16754	29384	2.12	2.7E-01	L77569.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
4980	17703		2.85	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 G10286 Homo sapiens cDNA
5011	17733	30339	2.53	2.7E-01	AA100656.1	EST_HUMAN	Z890a01.L1 Stratiene cdon (#837204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:365488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5011	17733	30340	2.53	2.7E-01	AA100656.1	EST_HUMAN	Z890a01.L1 Stratiene cdon (#837204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:365488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5185	17983	30509	2.39	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (HOXA-1.4)
5402	18202		0.85	2.7E-01	AB033171.1	NT	Astecpora mytilifera mitochondrial cyb gene for cytochrome b, partial cds
6249	19023	31995	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6249	19023	31998	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6515	19280	32282	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6515	19280	32283	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6881	19598	32637	2.23	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6916	19653	32689	0.56	2.7E-01	U15967.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
6952	19434		0.79	2.7E-01	AI540070.1	EST_HUMAN	cd08h08.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7256	19940	33015	0.74	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.8 KD PROTEIN B0563.3 IN CHROMOSOME X
7461	20134	33225	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7461	20134	33226	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7668	20266	33363	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7688	20256	33364	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7638	20303	33411	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7638	20303	33412	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7694	20358	33472	0.71	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
7763	20459	33583	0.89	2.7E-01	AA013147.1	EST_HUMAN	zs35b11.a1 Scores, retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element

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7925	20820		0.53	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.51	2.7E-01	R39257.1	EST_HUMAN	ye91h08.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8100	20884	34022	0.8	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8657	21349	34494	0.69	2.7E-01	Q14784	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21616	34760	0.46	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9232	21911	35084	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9235	21914		2	2.7E-01	P37826	SWISSPROT	FIMBRIAE W PROTEIN
9700	22351	35546	0.61	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9981	22629	35838	0.74	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus catgranulin C mRNA, partial cds
10018	22866	35982	3.09	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10149	22787	36012	0.57	2.7E-01	AF156639.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10149	22787	36013	0.57	2.7E-01	AF156639.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10714	23403	36642	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10714	23403	36643	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10724	23412	36853	3.13	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11820	24406		1.5	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12482	25180		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12665	24863		2.83	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12811	25054	30929	1.95	2.7E-01	AV742419.1	EST_HUMAN	AV742419 CB Homo sapiens cDNA clone CBMAXF02 5'
457	15542	25883	2.03	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
468	13254		1.38	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1372	14120	28795	1.65	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1417	14165	28848	1.14	2.6E-01	AB013290.1	NT	Glycine max pseudogene for B4 30K
1889	14626	27335	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1889	14628	27336	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04410.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb:M86072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactant protein 3 protein gene (MOUSE);
2086	14818		10.48	2.6E-01	AW733152.1	EST_HUMAN	
2148	14878	27613	3.7	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2476	15184		1.62	2.6E-01	Y12986.1	NT	B.martinius fcd. gene

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2548	16283		8.87	2.6E-01	BE272440.1	EST_HUMAN	60126016F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2990043 5'
3568	16323	28971	8.89	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3634	16387	29028	2.02	2.6E-01	AF228118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4079	16823	29449	0.96	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE: reserquenes, MAGF Homo sapiens cDNA
4134	16876	29506	16.7	2.6E-01	BE080568.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4324	17063	29691	1.2	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4459	17195	29821	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4459	17195	29822	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4511	17248	29881	1.46	2.6E-01	AA457617.1	EST_HUMAN	ea89d07.1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4601	17336	29965	1.77	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4687	17401	30035	1.18	2.6E-01	AF142703.1	NT	Oxythresia radiceosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4910	17638	30252	0.95	2.6E-01	AF153350.1	NT	Mus musculus metalloprotease disintegrin (Adam28) mRNA, complete cds
4914	17642	30257	3.6	2.6E-01	H04858.1	EST_HUMAN	y51605.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:152288 5'
6257	18063		1.06	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5484	18283		0.68	2.6E-01	AI862398.1	EST_HUMAN	td18a03.x1 NCL_CGAP_Cor16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element
5688	18481	31400	0.73	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor (GHM enhancer 3 genes, partial cds; and unknown g
5980	25417		2.35	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6108	18885	31854	2.26	2.6E-01	AI682557.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDFF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6108	18885	31855	2.26	2.6E-01	AI682557.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDFF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6328	19098	32086	0.91	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 67
6570	19334	32344	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938156 5'
6570	19334	32345	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938156 5'
6838	19673	32719	0.9	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);

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7289	19872	33050	0.62	2.6E-01	BE148361.1	EST_HUMAN	CMO-HT0245-031198-085-f04 HT0245 Homo sapiens cDNA
7329	25110		0.79	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
7363	20044		0.69	2.6E-01	AA196149.1	EST_HUMAN	zp92a01.11 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
7639	20304	33413	1.9	2.6E-01	R10395.1	EST_HUMAN	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128004 3' similar to gb:XI2517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7687	20351	33465	0.66	2.6E-01	Q09855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C28E6.01 IN CHROMOSOME I
7748	20444	33566	1.3	2.6E-01	R02411.1	EST_HUMAN	ye82a07.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
7804	20489	33620	1.15	2.6E-01	BE144331.1	EST_HUMAN	MR0-HT0166-181198-003-d12 HT0166 Homo sapiens cDNA
8040	20735	33867	0.64	2.6E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8040	20735	33868	0.64	2.6E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8232	20928	34064	3.05	2.6E-01	BF345588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150396 5'
8309	21003	34140	2.13	2.6E-01	Q10189	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8594	21286	34424	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8594	21286	34425	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9367	21942	35116	0.96	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9639	22291		0.62	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9768	22419	35628	1.19	2.6E-01	P97366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFFH-G)
9768	22419	35627	1.19	2.6E-01	P97366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFFH-G)
9930	22578		0.48	2.6E-01	U67581.1	NT	Methanococcus jannaschii section 123 of 160 of the complete genome
10090	22738		0.74	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10406	23052		0.9	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10467	23113		0.45	2.6E-01	AB015355.1	NT	Homo sapiens NRAM2 gene for natural resistance-associated macrophage protein 2, complete cds
11400	24006	37310	1.78	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11511	24111		68.41	2.6E-01	X61795.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11896	24534		1.71	2.6E-01	10180655	NT	Mus musculus Jerky (Jrk), mRNA
12177	25309		3.1	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12242	24683	31077	2.81	2.6E-01	AF316898.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced
12565	24895		1.56	2.6E-01	D88425.1	NT	Caria cobaya mRNA for serine/threonine kinase, complete cds
12725	24998		2.19	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
234	13045	25684	2.55	2.6E-01	4502286	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA

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235	13045	25884	2.39	2.5E-01	4502286	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
248	13057		3.32	2.5E-01	M26501.1	NT	Starfish (<i>P. ochraceus</i>) cytoplasmic actin gene, complete cds
813	13584	26250	1.35	2.5E-01	U09884.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapdh-S) gene, complete cds
1038	13798		1.2	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1089	13857	26517	6.42	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stratogene lung (#837210) Homo sapiens cDNA clone IMAGE:117488 5'
1509	14255	26941	0.9	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1721	14484		4.79	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1876	15581	27323	1.58	2.5E-01	BE69604.1	EST_HUMAN	PM4-CTD400-310700-005-008 CTD400 Homo sapiens cDNA
1876	15581	27324	1.58	2.5E-01	BE69604.1	EST_HUMAN	PM4-CTD400-310700-005-008 CTD400 Homo sapiens cDNA
2407	15128		18	2.5E-01	AE000675.1	NT	Aquifex acidicus section 7 of 109 of the complete genome
2500	15217		1.09	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3370	16128		0.84	2.5E-01	BF698193.1	EST_HUMAN	602125525F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4282279 5'
3407	16165		3.04	2.5E-01	AW973471.1	EST_HUMAN	EST386484 MAGE resequences, MAGM Homo sapiens cDNA
3524	16280	28935	1.25	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3537	16293	28942	7.54	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3828	16579	29211	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3828	16579	29212	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4283	17022		0.97	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4700	17434		1.25	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4706	17438	30070	3.99	2.5E-01	AF007788.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4732	17484	30101	2.01	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4751	17483		3.7	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4781	17513	30135	1.09	2.5E-01	BE696785.1	EST_HUMAN	601437498F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922600 5'
4887	17710	30315	0.71	2.5E-01	AW873588.1	EST_HUMAN	h62f11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041697 3' similar to WP:Y71F8A_294.D CE22859;
5243	18049	30878	13.48	2.5E-01	S63390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
5870	18657	31598	0.73	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5871	18658		0.98	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6529	19295	32299	0.95	2.5E-01	AJ251973.1	NT	Homo sapiens partial stearin-1 gene
6845	19427	32442	0.79	2.5E-01	8394138	NT	Rattus norvegicus rab3 (RABIN3), mRNA

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7252	19936	33011	0.88	2.5E-01	U13892.1	NT	Feline calicivirus CFI/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7278	19962		1.29	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7494	20167	33269	0.83	2.5E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7538	20206	33303	3.6	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7744	20440	33564	2.47	2.5E-01	BF109040.1	EST_HUMAN	757a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7764	20460	33674	0.8	2.5E-01	BE960712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826188 3'
8125	20819	33955	1.87	2.5E-01	BF038595.1	EST_HUMAN	601458238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862809 5'
8296	20960	34128	0.7	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8534	21228	34368	3.67	2.5E-01	H53236.1	EST_HUMAN	yq84f07.f1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202501 5'
8774	21498	34613	0.78	2.5E-01	M88628.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9416	22094	35265	15.72	2.5E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9416	22094	35268	15.72	2.5E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9472	22081	35253	2.08	2.5E-01	AF085164.1	NT	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
9472	22081	35254	2.08	2.5E-01	AF085164.1	NT	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
9908	22646	35858	1.39	2.5E-01	AW581987.1	EST_HUMAN	RC3-ST0186-130100-015-407 ST0186 Homo sapiens cDNA
							xy40c10.x1 NCJ_CGAP_U1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
10441	23087	36315	2.13	2.5E-01	AW152246.1	EST_HUMAN	Mouse L1Md LINE DNA
10444	23090	36319	1.21	2.5E-01	X58491.1	NT	Human mRNA for KIAA0124 gene, partial cds
11013	23685	36945	3.43	2.5E-01	D50914.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
11647	24244		1.61	2.5E-01	AF027153.1	NT	
11803	24393	37727	1.29	2.5E-01	U45315.1	NT	Lithosoides sigmoidonitis microfilarial sheath protein SHP-1a precursor (shp1a) gene, complete cds
11832	24490	37808	5.12	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
11960	25388		6.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12366	24768		1.37	2.5E-01	AF000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position (3/7)
12412	25233	30821	1.37	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
540	13323	25955	1.69	2.4E-01	AA936316.1	EST_HUMAN	on70d04.at Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
828	13698	26289	3.34	2.4E-01	BF578124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1281	14031	26700	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1281	14031	26701	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1363	14111	26785	1.03	2.4E-01	Y17293.1	NT	Homo sapiens FLJ-1 gene, partial
1843	14581		32.88	2.4E-01	AF26753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1893	14630	27340	1.33	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2134	14884	27694	1.1	2.4E-01	AF111198.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2165	14884		1.44	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAI PROTEASE)
2258	14885	27725	2.28	2.4E-01	AE000680.1	NT	Aquifex acidicus section 12 of 109 of the complete genome
2382	15104	27843	1.38	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NC1_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2539	15254	27894	2.46	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A;
2765	15470	28213	2.16	2.4E-01	X71783.1	NT	D.discoideum (Ax2-K) ponA gene
2789	15494	28234	2.84	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
							Bovine adenovirus 3 complete genome
3129	15894		2.04	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofitt (gag/pol) genes, complete cds
3145	15909	28554	1.48	2.4E-01	X74209.1	NT	H.sapiens AGT gene, Pad fragment of Intron 4
3743	18496	28131	0.73	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4010	18756		0.74	2.4E-01	D29360.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4883	17610		1.09	2.4E-01	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
4889	17712	30317	0.98	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5375	18175	30865	0.98	2.4E-01	AI925707.1	EST_HUMAN	wc33d05.x1 NC1_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2457128 3'
5376	18175	30866	0.98	2.4E-01	AI925707.1	EST_HUMAN	wc33d05.x1 NC1_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2457128 3'
5397	18197	30891	0.8	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5569	18368	31275	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5569	18368	31276	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5597	18392		0.77	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5799	25076		0.99	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
							754d04.x1 NC1_CGAP_Br18 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
							Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
5805	18596	31520	2.22	2.4E-01	BF592336.1	EST_HUMAN	
5895	18680	31627	3	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5899	18780	31741	2.83	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6050	18830	31793	0.67	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdAADE11 5'
							wc62c11.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
6441	19208	32206	2.23	2.4E-01	AI689889.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7243	18928	33004	9.5	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7404	20081	33163	0.55	2.4E-01	N48732.1	EST_HUMAN	yy55c11.r1 Scaree_multiple_sclerosis_21bHMSF Homo sapiens cDNA clone IMAGE:277490 5'
7625	20291	33400	0.91	2.4E-01	AF228644.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8247	20941	34078	1.61	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9497	21189	34332	1.02	2.4E-01	BF242784.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106288 5'
8552	21244		0.47	2.4E-01	BF678275.1	EST_HUMAN	602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9030	21720	34874	0.49	2.4E-01	AL138077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9030	21720	34875	0.49	2.4E-01	AL138077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9463	22013	35181	7.01	2.4E-01	AI693515.1	EST_HUMAN	wk43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330308 3' similar to contains MER22.b1 TAR1 repetitive element;
9603	22258	35441	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
9603	22258	35442	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10337	22884	36202	1.68	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10687	23358	36598	4.8	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
10739	23428	36671	1.39	2.4E-01	AF030189.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11158	23825		2.09	2.4E-01	Z21647.1	NT	P. asiatica mosaic virus genomic RNA
11840	24424	37765	1.32	2.4E-01	BE617638.1	EST_HUMAN	601441421T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846838 3'
11891	24461	37801	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D octo reductase (FOR) gene, exon 6
12019	25180		2.34	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12080	24588		2.74	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative me7 protein (me7 gene)
12287	25162		1.97	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12400	25201		2.08	2.4E-01	BF184542.1	EST_HUMAN	601842848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4063739 5'
12720	24982		3.66	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
380	13167	25810	1.08	2.3E-01	S75886.1	NT	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]
622	13401		6	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
662	13430	26069	33.31	2.3E-01	U67656.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
813	13680	26341	4.19	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1558	14305		1.12	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1589	14345	27035	1.23	2.3E-01	AJ245480.1	NT	Brassica napus sig gene for S-biosyn glycoprotein, cultivar T2
1628	14374	27063	2.74	2.3E-01	Y10897.2	NT	Mus musculus cdh5 gene, exon 1, partial
2038	14772		1.51	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4JFE1 gene
2447	15166	27803	2.66	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2657	15367	28105	1.59	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2827	14114	26789	3.38	2.3E-01	AB015033.1	NT	Marinibacteria agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2863	15729	28378	1.36	2.3E-01	AA601379.1	EST_HUMAN	no16d08.s1 NCI_QGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THIR repetitive element;
3082	15847		7.07	2.3E-01	R21732.1	EST_HUMAN	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3363	16122	28780	1.14	2.3E-01	H08836.1	EST_HUMAN	y97h10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3821	16573	29205	1.01	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic,
3914	16664		5.22	2.3E-01	7862133	NT	2212 nt, segment 1 of 3]
4316	17055	29880	1.1	2.3E-01	R82252.1	EST_HUMAN	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4368	17108		1.98	2.3E-01	L78789.1	NT	y1701.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4417	17163	29784	1.03	2.3E-01	D80899.1	NT	Mus musculus tenin (Ran-1c) gene, promoter region
4454	17190	29816	2.51	2.3E-01	AF082535.1	NT	Synechocystis sp. PCC8803 complete genome, 1/27, 1-133859
4517	17252	29887	6.19	2.3E-01	5031984	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4988	17711	30316	0.84	2.3E-01	AB032400.1	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5221	18028	30854	2.53	2.3E-01	AB040945.1	NT	Mus musculus tulip 1 mRNA, complete cds
							Homo sapiens mRNA for KIAA1512 protein, partial cds
5343	18146	30825	2.06	2.3E-01	BF086381.1	EST_HUMAN	7430408.x1 NCL CGAP_OV18 Homo sapiens cDNA clone IMAGE:3476899 3' similar to SW:GAG_SMSAV
5443	18242	31130	4.58	2.3E-01	X86687.1	NT	P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE
5563	18360		0.84	2.3E-01	L39112.1	NT	SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;
5665	18480	31374	0.76	2.3E-01	S80371.1	NT	C. familiaris rom1 gene
							Vitellogenin corneum small subunit ribosomal RNA gene
5851	18638	31575	1.59	2.3E-01	A1708840.1	EST_HUMAN	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
5851	18638	31575	1.59	2.3E-01	A1708840.1	EST_HUMAN	as27612.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238
6558	19323	32330	0.83	2.3E-01	AF198089.1	NT	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6778	19522	32549	4.33	2.3E-01	A1718148.1	EST_HUMAN	as27612.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238
7011	19703	32759	1.08	2.3E-01	8923323	NT	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7188	19874	32947	0.9	2.3E-01	AF000227.1	NT	as27612.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238
7315	19998	33077	3.14	2.3E-01	AF175398.1	NT	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7318	20001	33079	0.64	2.3E-01	AV719681.1	EST_HUMAN	Onychogadus cucullus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for
7318	20001	33080	0.64	2.3E-01	AV719681.1	EST_HUMAN	mitochondrial product
7508	20179		2.94	2.3E-01	6754779	NT	as4212.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu
7513	20184	33278	1.38	2.3E-01	BE888071.1	EST_HUMAN	repetitive element
7652	20316		2.73	2.3E-01	N80983.1	EST_HUMAN	Homo sapiens hypofibrinolytic protein FLJ20345 (FLJ20345), mRNA
7750	20446	33569	0.71	2.3E-01	AL161558.2	NT	Secale cereale omega secalin gene, complete cds

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7882	20587	33717	2.18	2.3E-01	M68831.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tet-alpha elanine version) gene, complete cds
8391	21084	34217	0.47	2.3E-01	U57988.1	NT	Mus musculus prosaposin (psap)SGP-1) gene, complete cds
8671	21363	34610	0.56	2.3E-01	AW090541.1	EST_HUMAN	xc90e06.x1 NC1_CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2591554 3'
8786	21478	34827	0.45	2.3E-01	AW864460.1	EST_HUMAN	EST376833 MAGE resequences, MACH Homo sapiens cDNA
9039	21729	34883	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (BB:X633368)
9039	21729	34884	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (BB:X633368)
9480	22133	35313	0.62	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9609	22262	35448	0.62	2.3E-01	U77674.1	NT	Tribolium castaneum transcription factor homolog (To-eve) gene, complete cds
9828	22281	35471	0.5	2.3E-01	BE277880.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2886739 5'
9882	22334	35529	0.59	2.3E-01	AW864460.1	EST_HUMAN	EST376833 MAGE resequences, MACH Homo sapiens cDNA
9731	22382	35584	1.02	2.3E-01	X62124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9767	22418	35625	0.58	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-261289-001-404 DT0036 Homo sapiens cDNA
9834	22485	35688	2.45	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
9892	22542	35734	2.75	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10340	22987	36205	0.84	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22988		5.11	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10937	23617	36867	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10937	23617	36868	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11144	23811	37092	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11144	23811	37093	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11324	24016	37318	3.03	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
11815	24403		1.75	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11855	24439		1.33	2.3E-01	6006010	NT	Homo sapiens Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA
12004	24539		4.47	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12088	24593		4.88	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M8 Homo sapiens cDNA clone HCOE44 5'
12120	24612		1.52	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b08 SN0012 Homo sapiens cDNA
12173	25319	30711	2.88	2.3E-01	AW903623.1	EST_HUMAN	xx21d07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q8Z175
12208	25368	30813	8.63	2.3E-01	BE882464.1	EST_HUMAN	Q62175 LYSYL OXIDASE-RELATED PROTEIN 2 ; contains PTR5.b2 TAR1 repetitive element ;
12255	24701		2.51	2.3E-01	BF663319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
							602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12303	24728		2.35	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12308	24784		1.76	2.3E-01	U49845.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12403	24728		1.55	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12647	24952		2	2.3E-01	BF475611.1	EST_HUMAN	nac38h12.x1 Lupakl_sciatic_ nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
88	12914	25552	1.63	2.2E-01	A052190.1	EST_HUMAN	ccz14et0.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1676290 3' similar to
1557	14304	26983	1.64	2.2E-01	AF167850.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2082	14814	27547	2.52	2.2E-01	M34840.1	NT	Homo sapiens PPAR delta gene, promoter region
2402	15123	27960	6.3	2.2E-01	BF677538.1	EST_HUMAN	Fresh-water sponge Enfi1 alpha collagen (COLF1) gene
2594	15308	28044	2.02	2.2E-01	BE618258.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249980 5'
2594	15308	28045	2.02	2.2E-01	BE618258.1	EST_HUMAN	601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866190 5'
2684	15651	28294	4.36	2.2E-01	BE155625.1	EST_HUMAN	601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866190 5'
2684	15651	28295	4.36	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0383-281299-003-e12 HT0353 Homo sapiens cDNA
2621	15687		1.57	2.2E-01	AF020503.1	NT	PM2-HT0353-281299-003-e12 HT0353 Homo sapiens cDNA
3387	16146		1.97	2.2E-01	AL161582.2	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3794	16546		1.12	2.2E-01	AF155728.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4105	16848		0.72	2.2E-01	U68174.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4194	16935	29562	6.45	2.2E-01	AF155142.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4232	16973	29597	2.11	2.2E-01	AF117340.1	NT	Mus musculus mbed kinase kinase 3 (Mik3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds
4232	16973	29598	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekd1) mRNA, complete cds
4323	17082	29689	1.21	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekd1) mRNA, complete cds
4323	17082	29690	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4775	17507		1.36	2.2E-01	D50804.1	NT	Human scRNA (BC200 beta) pseudogene
4779	17511	30133	2.1	2.2E-01	AA211218.1	EST_HUMAN	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4982	17705		1.1	2.2E-01	L13299.1	NT	zq87c05.1 Streptococcus hnt neuron (#837233) Homo sapiens cDNA clone IMAGE:648988 5'
5062	17781		0.93	2.2E-01	S57565.1	NT	Mus musculus vinculin gene, exon 3
5140	17858	30474	2.84	2.2E-01	5835974	NT	histamine H2-receptor [rat, Genomic, 1928 nt]
5059	18454	31368	2.07	2.2E-01	5803002	NT	Vidua chalybeata mitochondrion, complete genome
5669	18484		4.5	2.2E-01	ID64000.1	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5910	18694	31846	0.96	2.2E-01	U67087.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538989
5910	18694	31847	0.96	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx7) mRNA, complete cds
							Gallus gallus T-box containing protein (Ch-Tbx7) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6806	19369	32381	0.73	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
6826	19662	32708	10.21	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7029	19721	32777	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7029	19721	32778	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7181	19877	32950	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7191	19877	32951	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7386	20068	33144	0.63	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7628	20294	33402	0.68	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain: C-125
7819	20614	AF155143.1	2.04	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7887	20682	33808	1.01	2.2E-01	Z49933.1	NT	E. coli sepA and sepB genes
8449	21141	34279	0.64	2.2E-01	AJ132818.1	NT	Pan troglodytes MecP2 gene 3'UTR
8784	21486	34632	3.53	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
8920	21611		4.35	2.2E-01	AW855039.1	EST_HUMAN	PM8-GT0263-241289-009-007 GT0263 Homo sapiens cDNA
9013	21703	34853	1.45	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dera1), mRNA
9098	21788	34952	1.04	2.2E-01	BF378354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9189	21859	35024	1.36	2.2E-01	W02988.1	EST_HUMAN	z04f08.f1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:291591 5'
9207	22088	35259	13.43	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9252	21831	35104	0.69	2.2E-01	AJ008639.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xkpb3)
9263	22017	35185	0.81	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9276	22030	35200	3.95	2.2E-01	M89643.1	NT	Brachydanio rerio opendyrin beta and gamma chains (Epd) gene, complete cds
9521	22174	35358	0.58	2.2E-01	Q90880	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
9715	22868	35584	3.4	2.2E-01	AF197941.1	NT	Fusaria hygrogrametrica chloroplast-localized small heat shock protein (CP-HSP21) mRNA, complete cds; nuclear gene for chloroplast product
9853	22503	35703	1.85	2.2E-01	BF206507.1	EST_HUMAN	601809724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10076	22724	35941	0.95	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
10232	22880	36092	0.6	2.2E-01	T59472.1	EST_HUMAN	y663008.t1 Strabagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
10232	22880	36093	0.5	2.2E-01	T59472.1	EST_HUMAN	y663008.t1 Strabagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
10268	22816	36126	0.58	2.2E-01	AF068284.1	NT	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyruvate quinone synthase A (pqoA) genes, complete cds; and pyruvate quinone
10341	22888		0.61	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Pht1) gene, partial cds

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10387	23033	36247	0.6	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10387	23033	36248	0.6	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10520	23168	36394	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 1i and AS
11070	23740	37014	1.56	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11164	23831	37110	1.46	2.2E-01	AB021083.1	NT	TT virus ORF1 gene, isolate TS4-II, partial cds
11399	24005	37309	4.63	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11438	23205	36437	5.22	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51680), mRNA
11935	24493		1.66	2.2E-01	BE870859.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
12040	25380		2.21	2.2E-01	U82971.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), celltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LP
12123	24615		2.19	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12225	17804	30591	3.87	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12228	24681		1.6	2.2E-01	AW661922.1	EST_HUMAN	h17b02.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
12731	25371		2.88	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GK Hom sapiens cDNA clone GKCAH802 5'
950	13716	26382	2.12	2.1E-01	AA568289.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
953	13718	26384	0.77	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1102	13859		2.76	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1178	13928	26563	1.15	2.1E-01	6754289	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1176	13929	26564	1.15	2.1E-01	6754289	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1908	14843	27353	2.07	2.1E-01	AA908824.1	EST_HUMAN	ck73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2152	14862	27616	4.2	2.1E-01	BF695079.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN):
2485	15596	27942	1	2.1E-01	H73988.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247603 5'
2485	15596	27943	1	2.1E-01	H73988.1	EST_HUMAN	y004f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2556	15270	28005	0.91	2.1E-01	AF022814.1	NT	y004f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2925	15691	28335	2.3	2.1E-01	6812445	NT	Fugu rubripes transcription factor (SLP-1) and home-oxigenase genes, complete cds
3786	16538		6.08	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNIH4), mRNA
4032	16777	29408	1.1	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
4032	16777	29409	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4343	17082		1.77	2.1E-01	AB033041.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4537	17272	29904	1.23	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
5013	17734	30341	1.4	2.1E-01	IQ01338	SWISSPROT	Homo sapiens pshsp47 gene, complete cds
							ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)

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5090	17809	30426	1.09	2.1E-01	AE001628.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5218	18028	30650	0.24	2.1E-01	BF672895.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
6787	19631	32659	1.4	2.1E-01	AJ223392.1	NT	Dolo fragilis mitochondrial 16S rRNA gene, partial
6798	19469	32481	1.82	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7308	19889	33085	0.85	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7308	19889	33088	0.85	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7317	20000		2.38	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7806	20272	33380	1.84	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT19) gene, complete cds
7851	20315	33425	1.22	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7851	20316	33428	1.22	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7971	20668		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8400	21083	34229	4.44	2.1E-01	U88399.1	NT	Haemophilus influenzae hmcD, putative haemochrom processing protein (hmcC), putative ABC transporter (hmcB), putative haemochrom structural protein (hmcA), and haemochrom immunity protein (hmcI) genes, complete cds
8696	21388	34531	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
8696	21388	34532	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
8857	21548		0.45	2.1E-01	AB022524.1	NT	Homo sapiens APCL gene, exon 9
8936	21628	34768	5.68	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
9404	22068	35237	0.57	2.1E-01	N42536.1	EST_HUMAN	y11e10J1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954 5'
9404	22068	35238	0.57	2.1E-01	N42536.1	EST_HUMAN	y11e10J1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954 5'
9413	22091	35282	2.31	2.1E-01	X97378.1	NT	A.thaliana mRNA for AtRanBP1b protein
9518	22171	35354	1.13	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10227	22875	36088	1.47	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10258	22908	36118	2.5	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10284	22812	36122	0.97	2.1E-01	BF574254.1	EST_HUMAN	(80 KD DIACYLGLYCEROL KINASE)
11554	24153		2.19	2.1E-01	11036847	NT	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11572	24171	37487	1.59	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11870	24944		1.38	2.1E-01	X57824.1	NT	RC3-HT0822-040500-013-b11 HT0822 Homo sapiens cDNA
12371	24775		2.07	2.1E-01	AF217490.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12578	25287		1.47	2.1E-01	L32588.1	NT	Homo sapiens fragile 16D alpha reductase (F-OR) gene, exons 8, 9, and partial cds
12635	24935		1.42	2.1E-01	BE622149.1	EST_HUMAN	Human granulosa gene
							601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12758	25019	30960	1.79	2.1E-01	BE672330.1	EST_HUMAN	7a59e02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3223034 3'
195	13008	25660	2.43	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for arena, complete cds
521	13305		3.11	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
683	13459	26103	1.24	2.0E-01	MT7085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VHα2
782	13584	26225	2.19	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
991	13753	26414	1.09	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781448-920915
1103	13860	26519	2.47	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1232	13981	26561	1.77	2.0E-01	AJ132895.6	NT	Homo sapiens rac1 gene
1285	14035	26706	1.63	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-281289-002-c08 HT0422 Homo sapiens cDNA
1443	14180		1.52	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1470	14217	26804	14.63	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1544	14280	26977	1.97	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0605
1550	14296	26983	1.01	2.0E-01	AF280700.1	NT	Homo sapiens sodium/folate symporter mRNA, partial cds
1692	14436	27132	1.4	2.0E-01	U23346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1712	14455		1.87	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds; and unknown gene
1752	14494		4.33	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1883	14620	27329	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1883	14620	27330	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2347	15070		1.63	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
3555	16310		0.71	2.0E-01	AW238005.1	EST_HUMAN	xp15502.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3693	16447	29087	0.89	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
3822	16574	29208	1.12	2.0E-01	AL163204.2	NT	CED-11 PROTEIN
3936	16686	29327	0.76	2.0E-01	Z46906.1	NT	Homo sapiens chromosome 21 segment HS21C004
4528	17263		8.49	2.0E-01	BE828165.1	EST_HUMAN	Sus scrofa
4979	17702	30309	5.26	2.0E-01	8922080	NT	QV4-EN0032-180500-223-e03 EN0032 Homo sapiens cDNA
5009	16237	28883	0.8	2.0E-01	P46607	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5359	18161	30845	2.63	2.0E-01	X55600.1	NT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5655	18450	31363	1.94	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5750	18542	31484	0.76	2.0E-01	X91866.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5969	18751	31712	6.3	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6081	18860		0.73	2.0E-01	M75987.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6192	18968	31943	0.79	2.0E-01	P02467	SWISSPROT	Human hepatocyte growth factor gene, exon 1
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6335	19105	32094	3.2	2.0E-01	X61033.1	NT	Mauratus mu class glutathione transferase gene
6435	19203	32200	4.02	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141088-001-g08 CT0247 Homo sapiens cDNA
7194	19880	32954	1.28	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkc) gene, exons 3 through 7
7345	20026	33102	0.68	2.0E-01	P54422	SWISSPROT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
7676	20339	33452	0.84	2.0E-01	V00728.1	NT	Mouse germ line gene coding for beta-globin (Y2)
7853	20548		5.8	2.0E-01	AF028028.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8100	20794	33825	2.85	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8624	21316		0.89	2.0E-01	BE562247.1	EST_HUMAN	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9251	21930	35103	0.82	2.0E-01	U82511.1	NT	Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds
9280	21957	35129	0.68	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9458	22008		4.97	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9646	22298	35493	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9646	22298	35494	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9791	22442		2.11	2.0E-01	AF146682.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9941	22589	35762	1.98	2.0E-01	AF086807.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9941	22589	35793	1.98	2.0E-01	AF086807.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10067	22715	35933	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10067	22715	35934	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10114	22762		0.69	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10305	22952	36167	2.78	2.0E-01	X97121.1	NT	R.novogicus mRNA for NTR2 receptor
10744	23431	36674	1.66	2.0E-01	D89088.1	NT	Salvelinus pinus mRNA for transferrin, complete cds
10744	23431	36675	1.66	2.0E-01	D89088.1	NT	Salvelinus pinus mRNA for transferrin, complete cds
11609	24207	37530	1.4	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
11609	24207	37531	1.4	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12358	24762		1.61	2.0E-01	AF206637.2	NT	Plimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12545	25210		1.39	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12556	25139	30894	1.38	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12594	24950	30985	3.58	2.0E-01	A023582.1	EST_HUMAN	0680410.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1843610 3'
12618	24924		2.68	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
12753	25014	30978	1.87	2.0E-01	11528495	NT	Mus musculus fructoseamine 3 kinase (Fn3k), mRNA
103	12929		3.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
342	13143	25781	6.86	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
641	13420	28058	1.43	1.9E-01	U32581.2	NT	Homo sapiens lamda1fota protein kinase C-interacting protein mRNA, complete cds
641	13420	28059	1.43	1.9E-01	U32581.2	NT	Homo sapiens lamda1fota protein kinase C-interacting protein mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
648	13427	28068	5.97	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
649	13427	28068	8.46	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
965	13730		1.73	1.9E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1082	13840	28499	13.43	1.9E-01	AA558813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1349	14087	28772	1.76	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1414	14162		2.51	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocytes binding protein-2 (rbp-2) gene, complete cds
2380	15102	27841	3.61	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2823	15689	28333	3.43	1.9E-01	U60080.1	NT	Sigmoidon hispidus p53 gene, partial cds
2939	15704		5.68	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (V) gene, complete cds
3002	15768	28417	0.95	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3330	16149	28803	4.28	1.9E-01	D73197.1	NT	Mouse gene for Immunoglobulin diversity region D1
3473	16229	28883	4.44	1.9E-01	R16467.1	EST_HUMAN	y42710.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:128547 5'
3816	16568	29109	1.33	1.9E-01	P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3973	16722	29356	3.15	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4063	16808	28438	1.28	1.9E-01	AW754108.1	EST_HUMAN	CM3-CT0315-271189-045-b11 CT0315 Homo sapiens cDNA
4206	16847	29573	1.09	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
4950	17677		1.05	1.9E-01	AF223942.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5517	18315		4.88	1.9E-01	AW130149.1	EST_HUMAN	x728a07.x1 NCL CGAP_U01 Homo sapiens cDNA clone IMAGE:2618444 3' similar to gb:MF73779 RETINOIC
5558	18355	31265	7.87	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
5749	18541	31463	0.7	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5795	18586		2.58	1.9E-01	AU733116.1	EST_HUMAN	Mus musculus Wrm protein (Wrm) gene, complete cds
6235	19009	31985	0.75	1.9E-01	AI762381.1	EST_HUMAN	AU733116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6294	19067	32050	1.03	1.9E-01	AW148452.1	EST_HUMAN	w154h02.x1 NCL CGAP_C016 Homo sapiens cDNA clone IMAGE:2394099 3'
6876	17952	30548	1.68	1.9E-01	R43212.1	EST_HUMAN	x14408.x1 NCL CGAP_K048 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP
6900	18638	32682	0.69	1.9E-01	AF034920.1	NT	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
6900	18638	32683	0.69	1.9E-01	AF034920.1	NT	yg09a12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31683 3' similar to contains MER13
7160	18847	32917	0.62	1.9E-01	U73846.1	NT	repetitive element;
7391	20070	33149	1.38	1.9E-01	U60922.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7436	20113	33201	3.11	1.9E-01	AF072724.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7885	20580	33709	1.46	1.9E-01	AL161557.2	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
8586	21278	34417	10.77	1.9E-01	AB033024.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
							Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
							Arabidopsis thaliana DNA chromosome 4, config fragment No. 57
							Homo sapiens mRNA for KIAA1198 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21638	34681	1.24	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8844	21536	34682	1.24	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9776	22428	36632	0.61	1.9E-01	AA912488.1	EST_HUMAN	cd86g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element
10142	22780	36005	0.85	1.9E-01	BE630353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10142	22780	36006	0.85	1.9E-01	BE630353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10540	23237	36470	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10540	23237	36471	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10655	23346	36583	2.09	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10886	23661	36915	1.34	1.9E-01	AA912480.1	EST_HUMAN	cd86f02.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gb:U21698_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element
10886	23661	36916	1.34	1.9E-01	AA912480.1	EST_HUMAN	cd86f02.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gb:U21698_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element
11487	24088	37369	1.63	1.9E-01	M22283.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
11726	24320	37845	2.77	1.9E-01	AL243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11752	24343	37673	1.6	1.9E-01	L07344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end
11847	24431	37772	1.3	1.9E-01	AF287263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
12389	24785		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
30	12858	25475	2.61	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
253	15539	25700	0.9	1.8E-01	AB022090.1	NT	Mus musculus Ctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
361	13159	25802	1.76	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	13503	26158	1.01	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
961	13728	26390	0.94	1.8E-01	AI912212.1	EST_HUMAN	wd71602.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1069	13826	26495	1.63	1.8E-01	AF000580.1	NT	Dicotyledonum discoidium plasmid Ddp5, complete genome
1288	14015	26683	8.26	1.8E-01	AL117188.1	NT	Yersinia pestis plasmid pCD1
1492	14239	26825	1.97	1.8E-01	6763947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1492	14239	26826	1.97	1.8E-01	6763947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1839	14577		1.2	1.8E-01	4508036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1859	14597		1.68	1.8E-01	AI733708.1	EST_HUMAN	cg22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1908	14645	27355	1.75	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya18-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2697	15406		2.36	1.8E-01	AW693728.1	EST_HUMAN	QV3-DT0018-081289-038-g04 DT0018 Homo sapiens cDNA
2698	15665		1.89	1.8E-01	AF184589.1	NT	Jonopsidium aculea LEAFY protein (LEAFY2) gene, partial cds
2904	15670	28319	1.29	1.8E-01	AW182300.1	EST_HUMAN	y41a03.x1 Soares_NFL_I_G8C_S1 Homo sapiens cDNA clone IMAGE:2659759 3'
3121	15986	28526	1.78	1.8E-01	AW695178.1	EST_HUMAN	QV0-BN0041-070300-147-g04 BN0041 Homo sapiens cDNA
3610	16363	28005	0.88	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3610	16363	28006	0.88	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4289	17038		1.43	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DOB), complete cds
4519	17254	28888	5.94	1.8E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4721	17453	30087	2.0	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya18-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4754	17466	30114	0.94	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4984	17707	30311	2.03	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151289-112-g08 ST0203 Homo sapiens cDNA
4999	17722	30325	1.06	1.8E-01	AI792382.1	EST_HUMAN	an28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5035	17754	30367	4.68	1.8E-01	AF161258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5718	18510	31431	0.82	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5835	18624	31558	0.68	1.8E-01	N28829.1	EST_HUMAN	y338h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264083 5'
6037	18817	31777	1.18	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Tra6), mRNA
6037	18817	31778	1.18	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Tra6), mRNA
6419	19187	32185	1.15	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6463	19230		2.06	1.8E-01	N94853.1	EST_HUMAN	y62h02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
6806	19644	32689	1.18	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for vsus, complete cds
6806	19644	32690	1.18	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for vsus, complete cds
7346	20027	33103	0.7	1.8E-01	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
9242	21921	35091	1.23	1.8E-01	MF73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9274	22028	35198	1.22	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9391	22053		0.5	1.8E-01	AA493751.1	EST_HUMAN	nh02a05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:949088 similar to contains L1. L1 repetitive element
9473	22126	35303	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9473	22126	35306	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35348	0.91	1.8E-01	M26019.1	NT	S.commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9514	22167	35349	0.91	1.8E-01	M26019.1	NT	S.commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9679	22331	35526	0.75	1.8E-01	P06123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9683	22335	35530	0.77	1.8E-01	U07548.1	NT	Methanococcus jannaschii section 80 of 150 of the complete genome
10033	22681		0.78	1.8E-01	AF200252.1	NT	Aquarius ampplus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10268	22814	36124	1.48	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10533	23230	36465	3.08	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10577	23272	36508	7.28	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysis genes, complete cds
10637	19644	32689	2.61	1.8E-01	AB018561.1	NT	Citrus latatus mRNA for vsus, complete cds
10637	19644	32690	2.61	1.8E-01	AB018561.1	NT	Citrus latatus mRNA for vsus, complete cds
10638	23329	36567	5.69	1.8E-01	AF019107.1	NT	Dicystostellum discoideum unknown (DGT041) gene, complete cds
10942	23621	36870	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11439	23206	36438	4.04	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
11767	24358	37691	3.45	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tx2r), mRNA
11987	24514		1.59	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12025	24553	31111	2.04	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4155318 5'
12476	24639		3.28	1.8E-01	Q96882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12585	24908		1.91	1.8E-01	R24494.1	EST_HUMAN	Yf48h10.1 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133027 5'
12628	24931		2.3	1.8E-01	Y11114.1	NT	E.coli mRNA for hexokinase (hok1)
12745	25324		1.61	1.8E-01	X18635.1	NT	Rattus norvegicus CaBP9k gene
563	13345	25972	1.57	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
787	13559	26221	2.32	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core Histones H2A, H2B, H3 and H4
941	13708		2.21	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1036	13798	26455	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1036	13798	26456	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1974	14710		2.6	1.7E-01	AF256051.1	NT	Homo sapiens BINIP3H (BINIP3H) gene, complete cds; nuclear gene for mitochondrial product
2863	15631	28276	2.29	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2863	15631	28276	2.29	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2927	15693	28339	1.55	1.7E-01	AA336909.1	EST_HUMAN	EST141951 Endometrial tumor Homo sapiens cDNA 5' end
2995	15761	28409	1.33	1.7E-01	AJ238738.1	NT	Naja naja atra cbt-1 gene, exons 1-3
2995	15761	28410	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cbt-1 gene, exons 1-3
3103	15868	28508	1.24	1.7E-01	AF081514.1	NT	Tenax canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3439	16195	28845	1.74	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3695	16348	28989	1.04	1.7E-01	AJ224877.1	NT	Homo sapiens hsp1 gene, complete CDS
3616	16389		0.82	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3918	16888	29309	4.84	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4522	17257		1.69	1.7E-01	X52836.1	NT	Schistosoma gregaria alpha repetitive DNA
4787	17518	30140	1.08	1.7E-01	AI247635.1	EST_HUMAN	qh57c09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element:
5054	17773		1.11	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1lb (ae) gene, complete cds
5122	17840	30456	0.75	1.7E-01	D37851.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5323	18128	30795	2	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:881088 3' similar to gbctM17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5323	18128	30796	2	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:881088 3' similar to gbctM17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5506	18304	31205	0.62	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6237	19011	31986	13.23	1.7E-01	H72118.1	EST_HUMAN	ys02g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6293	19066	32048	0.97	1.7E-01	AI370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6293	19066	32049	0.97	1.7E-01	AI370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6753	17822	30557	0.65	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
6760	19524		2.28	1.7E-01	AF028552.3	NT	Mesocricetus auratus oxiductin precursor (OVI) gene, complete cds
6802	19840		0.88	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7120	19808	32874	1.1	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7197	19883	32957	8.8	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7980	20060	33139	1.37	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7996	25112	33153	0.71	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
7760	20456	33580	1.32	1.7E-01	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7863	20558	33684	0.82	1.7E-01	AF150688.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8175	20869	34001	6.19	1.7E-01	7706428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8175	20869	34002	6.19	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8598	21290	34431	0.47	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8628	21320	34482	2.09	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
8743	21435	34580	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8743	21435	34581	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9068	21755	34916	0.48	1.7E-01	BE253142.1	EST_HUMAN	601118672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9068	21755	34917	0.48	1.7E-01	BE253142.1	EST_HUMAN	601118672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9490	22143	35323	7.85	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9597	22250	35435	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGE resequences, MAGO Homo sapiens cDNA
9597	22250	35438	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGE resequences, MAGO Homo sapiens cDNA
9815	22268	35455	3.14	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9708	22359	35555	0.63	1.7E-01	AL251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10133	22781		2.4	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10283	22940	36154	1.4	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10285	22942	36156	1.72	1.7E-01	AA627872.1	EST_HUMAN	nc60e07.s1 NCI_CGAP_Cc9 Homo sapiens cDNA clone IMAGE:1148282 3' similar to gbl.25081
10501	23147		0.45	1.7E-01	AL161542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN); Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42
10579	23274	36511	8.78	1.7E-01	BE360835.1	EST_HUMAN	601288547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
10709	23398	36637	2.65	1.7E-01	AA814617.1	EST_HUMAN	of43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426824 3'
11055	23725	36995	9.13	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11055	23725	36998	9.13	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11146	23813	37098	1.62	1.7E-01	Y08391.1	NT	S.pombe pap1+ gene
11348	24038	37341	1.69	1.7E-01	AA863375.1	EST_HUMAN	al45f08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
11712	24307		1.83	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
11746	24337	37663	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
11746	24337	37664	1.62	1.7E-01	P55899	SWISSPROT	(IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
11874	24453	37789	2.62	1.7E-01	11418157	NT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
12000	25320		1.95	1.7E-01	AL163278.2	NT	(IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
							Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
							Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12268	25167		1.65	1.7E-01	AI824404.1	EST_HUMAN	b68g05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M79779 RETINOIC
12562	24889	30908	16.27	1.7E-01	U01317.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
122	12940	25582	2.38	1.6E-01	AF217532.1	NT	Human beta globin region on chromosome 11
604	15518	26081	1.51	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1493	14240	26927	1.16	1.6E-01	AA548863.1	EST_HUMAN	y175f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135569 5'
1612	14258	26944	3.82	1.6E-01	AF268117.1	NT	nt28d12.st1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014839 3'
1917	14654	27364	1.86	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
1977	14713		1.51	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2383	15593	27844	1.36	1.6E-01	X94292.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2497	15214	27857	1.4	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2894	15681	28307	10.17	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2894	15661	28308	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29019	1.21	1.6E-01	AJ003165.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29019	1.21	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3682	16730		2.49	1.6E-01	AE004413.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
4294	17033	29681	9.42	1.6E-01	AF179680.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4423	17159		3.07	1.6E-01	AW968601.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
4431	17167		4.35	1.6E-01	6753319	NT	ESTS80677 IMAGE resequences, MAGJ Homo sapiens cDNA
4669	17598	30219	0.7	1.6E-01	P40631	SWISSPROT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4892	17619	30237	1.38	1.6E-01	AA088343.1	EST_HUMAN	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MILC LH) [CONTAINS: LINKER HISTONE
4911	17639	30253	1.54	1.6E-01	AJ006356.1	NT	PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4911	17639	30254	1.54	1.6E-01	AJ006356.1	NT	z84h08.a1 Stragene cdon (#637204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5303	18108	30768	0.99	1.6E-01	L40608.1	NT	E221955 38,865 BP SEGMENT OF CHROMOSOME XIV.;
5435	18234	30947	2.95	1.6E-01	AW197496.1	EST_HUMAN	Lycopodium esculentum RsaI fragment 2, satellite region
5435	18234	30948	2.95	1.6E-01	AW197496.1	EST_HUMAN	Lycopodium esculentum RsaI fragment 2, satellite region
5447	18248	31134	2.15	1.6E-01	AF034718.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5938	18720	31679	0.83	1.6E-01	BE028303.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O76984 O76984
6162	18939	31909	0.71	1.6E-01	BF183584.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
6162	18939	31910	0.71	1.6E-01	BF183584.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O76984 O76984
							HYPOTHETICAL 127.6 KD PROTEIN;
							Rattus norvegicus GCAA1 enhancer binding protein epsilon (cabepe) gene, complete cds
							RC3-BIN0034-310800-113-h01 BN0034 Homo sapiens cDNA
							601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
							601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6334	19104	32082	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 84
6334	19104	32083	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 84
6885	19802	32641	0.55	1.6E-01	AA398047.1	EST_HUMAN	Z889404.r1 Soares_tesis_NHT Homo sapiens cDNA clone IMAGE:729511 5'
6967	17844	30539	5.32	1.6E-01	AW281215.1	EST_HUMAN	UI-H-B12-agi-b-06-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7678	20340	33453	1.86	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7703	20366		0.74	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
7768	20464	33589	1.81	1.6E-01	L46349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7924	20619		0.51	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP1E0607 cDNA clone TCBAP0607
8018	20713	33844	0.87	1.6E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (cbbA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8530	21222	34364	0.88	1.6E-01	Z98119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2987771 to 3213410
8726	21417	34561	0.63	1.6E-01	R13673.1	EST_HUMAN	y60108.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
8831	21523		0.59	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8870	21561	34706	1.72	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001W
9009	21699		0.83	1.6E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9551	22204		2.09	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041189-011-h01 ST0200 Homo sapiens cDNA
9554	22207	35391	1.7	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001W
9589	22242		0.97	1.6E-01	BE155684.1	EST_HUMAN	PM2-HT0363-270100-004-f11 HT0363 Homo sapiens cDNA
10553	23249	36488	3.3	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-11189-028-G01 CT0220 Homo sapiens cDNA
10918	23598	36845	1.59	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10918	23598	36846	1.59	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10923	23603	36852	1.55	1.6E-01	BE259949.1	EST_HUMAN	601145789F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11059	23729		4.28	1.6E-01	AF106084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11388	23694	37298	7.28	1.6E-01	6871562	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11706	24301		1.28	1.6E-01	BF52737.1	EST_HUMAN	602039465F2 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4177073 5'
11888	25331		1.64	1.6E-01	6879466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
12002	24538	37273	5.28	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GCEMF07 5'
12292	24721	31052	1.72	1.6E-01	L14833.1	NT	Rat convertase PC5 mRNA, 5' end
12321	24740		1.5	1.6E-01	AW839711.1	EST_HUMAN	RG1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12418	26149		287.78	1.6E-01	AB046310.1	NT	Cucumis sativus KS mRNA for ent-kaurane synthase, complete cds
12574	24901		2.4	1.6E-01	AK024486.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12661	24961		1.72	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12687	24973	30892	1.7	1.6E-01	85066522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12796	25046		1.52	1.6E-01	BF672698.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283145 5'
241	13050	25689	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
241	13050	25690	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
573	15517		8.31	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
766	13539	26188	1.09	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1070	13828	26487	1.01	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1076	13833	26491	2.75	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1091	13849		1.42	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1194	13946	26610	0.82	1.5E-01	AW195516.1	EST_HUMAN	xt39411.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2698085 3'
1252	14001	26668	2.96	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
1252	14001	26669	2.96	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)
1465	14212	26901	1.86	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1901	14638	27347	1	1.5E-01	AW444451.1	EST_HUMAN	UI-H-B3-akb-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'
2716	15423	28162	1.98	1.5E-01	BF693361.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2914	15680		1.15	1.5E-01	AW572516.1	EST_HUMAN	xs56a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:U55072_ma1
3048	15814	28459	0.74	1.5E-01	O76687	SWISSPROT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3347	16106	28761	5.08	1.5E-01	AA835049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3361	16120	28777	0.82	1.5E-01	Z23104.1	NT	068805.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3361	16120	28778	0.82	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
							L. stagnalis mRNA for G protein-coupled receptor
							L. stagnalis mRNA for G protein-coupled receptor
3798	16491	29126	2.11	1.5E-01	U09884.1	NT	Mus musculus [CR/Swiss] glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3752	16504	29140	0.74	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3848	16599	29238	2.65	1.5E-01	AW665993.1	EST_HUMAN	h10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
4028	16773	29405	1.1	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191098-012-c09 HT0149 Homo sapiens cDNA
4161	16901	29530	8.35	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4676	17410	30046	1.67	1.5E-01	BF687665.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086223 5'
4703	15423	28162	1.92	1.5E-01	BF693361.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5132	17650	30467	1.55	1.5E-01	Z72808.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL086w

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5145	17864	30480	1.05	1.5E-01	AF056313.1	NT	Morone saxatilis gonadotropin-releasing hormone type II gene, complete cds
5175	17884	30489	2.16	1.5E-01	P07998	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5203	18011	30532	1.15	1.5E-01	AF256852.1	NT	Calman crocodilus MHC class II beta chain (hcIbeta) gene, complete cds
5245	18051		6.92	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5451	18250	31139	5.08	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-084-F10 CT0219 Homo sapiens cDNA
5492	18281	31188	8.42	1.5E-01	U65018.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5492	18281	31189	8.42	1.5E-01	U65018.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5915	18700	31663	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5915	18700	31664	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5952	18734	31693	1.93	1.5E-01	A1278505.1	NT	Mus musculus genomic fragment, 278 Kb, chromosome 7
6102	18880	31847	3.1	1.5E-01	BE727898.1	EST_HUMAN	601684322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833081 5'
6162	18929		1.77	1.5E-01	4508396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6251	19025	31989	2.09	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6409	25089	32176	2.21	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6437	19205	32201	4.99	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (O5ORF3), mRNA
6448	19216	32214	1.95	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6493	19259	32260	2.95	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6585	18348	32361	1.25	1.5E-01	AA714780.1	EST_HUMAN	mw30d10.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241971 3'
6612	18375	32389	1.66	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6882	17958	30554	6.82	1.5E-01	AW970285.1	EST_HUMAN	EST382378 MAGE resequences, MAGK Homo sapiens cDNA
6918	25102		0.79	1.5E-01	AA811545.1	EST_HUMAN	cb73f02.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element
7115	18903		2.07	1.5E-01	AF210842.1	NT	LTR2 repetitive element;
7290	18973	33051	2.86	1.5E-01	A1973157.1	EST_HUMAN	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7490	20102	33254	2.04	1.5E-01	AF299073.1	NT	wf52c08.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
7490	20162	33255	2.04	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7499	20171	33262	2.04	1.5E-01	AF500611.1	EST_HUMAN	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7499	20171	33263	2.04	1.5E-01	AF500611.1	EST_HUMAN	UIHIF-BNO-akk-d-05-0-UI1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7640	20305	33414	0.81	1.5E-01	U46660.1	NT	UIHIF-BNO-akk-d-05-0-UI1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7957	20652	33775	0.96	1.5E-01	P21303	SWISSPROT	Saccharomyces cerevisiae weak multifcopy suppressor of los1-1 (SOL3) gene, complete cds
							MEROZOITE RECEPTOR PK68 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8118	20812	33947	1.13	1.5E-01	AA970317.1	EST_HUMAN	cc85g12.a1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8211	20905		0.95	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8299	20993		11.54	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8332	21025	34162	1.6	1.5E-01	IL27635.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-529109 5'
8491	21183	34325	1.65	1.5E-01	D84476.1	NT	Panglossanodon gigas growth hormone (GH) mRNA, complete cds
8512	21204		0.71	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8737	21429	34575	1.18	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9002	21692	34842	2.88	1.5E-01	N74228.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9092	21781	34945	1	1.5E-01	BF585465.1	EST_HUMAN	z859e06.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296888 3' similar to
9100	21788		2.3	1.5E-01	AV754819.1	EST_HUMAN	PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9305	21972		0.74	1.5E-01	AU130007.1	EST_HUMAN	GVO000404 Human Psoarasis Differential Display/Homo sapiens cDNA
9353	20424	33543	7.32	1.5E-01	U00455.1	NT	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9717	22368	35568	0.53	1.5E-01	M77144.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9821	22472	35674	7.61	1.5E-01	AF007570.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
9821	22472	35675	7.51	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10103	22751	35965	2.92	1.5E-01	X98852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10207	22855	36070	2.16	1.5E-01	A1814046.1	EST_HUMAN	Aplysia californica carboxypeptidase D mRNA, complete cds
10207	22855	36071		1.5E-01	A1814046.1	EST_HUMAN	P.lentusculus mRNA for Integrin beta subunit
10285	22933	36148	2.01	1.5E-01	U40832.1	NT	wk53h12.x1 NCI_CGAP_Py22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10438	23084	36311	1.43	1.5E-01	AJ011884.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10438	23084	36312	1.43	1.5E-01	AJ011884.1	NT	wk53h12.x1 NCI_CGAP_Py22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10595	23289	36526	1.62	1.5E-01	BE088492.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10595	23289	36527	1.62	1.5E-01	BE088492.1	EST_HUMAN	Danio rerio transcription factor Pax6b (Pax6) mRNA, complete cds
10726	23414	36654	7.31	1.5E-01	AL163280.2	NT	Claviceps purpurea ps1 gene
10726	23414	36655	7.31	1.5E-01	AL163280.2	NT	Claviceps purpurea ps1 gene
10898	23576		1.7	1.5E-01	AB042975.1	NT	GM2-BT0688-210300-122-F11 BT0688 Homo sapiens cDNA
11012	23684	36944	1.6	1.5E-01	AW841915.1	EST_HUMAN	GM2-BT0688-210300-122-F11 BT0688 Homo sapiens cDNA
11057	23727	36999	1.95	1.5E-01	AA425488.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C080
							Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
							IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
							zw46d02.L1 Soares total_fetus_Nb24IF9_9w Homo sapiens cDNA clone IMAGE:773091 5' similar to
							contains element MER22 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11119	18973	33051	1.58	1.5E-01	AI873157.1	EST_HUMAN	wf5208.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2491310 3'
11625	24222		1.58	1.5E-01	AI193704.1	EST_HUMAN	q972601.x1 Soares fetal lung Nhlh19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to
11659	25202		11.07	1.5E-01	BF700682.1	EST_HUMAN	gbtM17897 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12320	24739		1.37	1.5E-01	AF030358.2	NT	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12324	24743		1.77	1.5E-01	AJ238332.1	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
						NT	Mus musculus mRNA for death inducer-obliterator-1 (Dio-1)
12369	24771		5.35	1.5E-01	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12385	25220		9.97	1.5E-01	R83077.1	EST_HUMAN	y087604.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194430 5'
12472	25241		2.53	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
12573	25150	30897	9.2	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
12783	25036	30865	1.89	1.5E-01	AJ278242.1	NT	Sus scrofa mRNA for sodium iodide symporter
292	13098		1.72	1.4E-01	AF006663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
880	13659		3.62	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1236	13985		2.48	1.4E-01	T81894.1	EST_HUMAN	y054c01.st Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:112032 3'
1742	14484		1.5	1.4E-01	6878980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1745	14487	27186	1.71	1.4E-01	AE007170.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1898	14635		0.98	1.4E-01	AW135741.1	EST_HUMAN	UH-HB1-act-a-09-0-J1.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1978	14714		9.33	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2478	15198	27835	1.38	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2795	15500	28241	4.23	1.4E-01	A183498.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3879	16629	29267	0.96	1.4E-01	R59232.1	EST_HUMAN	y97e03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3879	16629	29268	0.96	1.4E-01	R59232.1	EST_HUMAN	y97e03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4153	16895	29524	8.69	1.4E-01	A1699094.1	EST_HUMAN	b556c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4153	16895	29525	8.69	1.4E-01	A1699094.1	EST_HUMAN	b556c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4212	16953	29577	3.73	1.4E-01	AE007170.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
5014	17735	30342	0.94	1.4E-01	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5223	18030	30656	5.48	1.4E-01	T90677.1	EST_HUMAN	ye15c11.st Stratiotes lung (#637210) Homo sapiens cDNA clone IMAGE:117812 3'
5246	18052	30679	4.6	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5246	18052	30680	4.6	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6205	18980	31859	3	1.4E-01	BE326891.1	EST_HUMAN	h167c02.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3133538 3'
6391	19160	32160	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6391	19160	32161	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6477	19244	32244	3.14	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6490	19257		1.64	1.4E-01	BE266536.1	EST_HUMAN	601183523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6509	19274	32275	2.45	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7026	19718		0.65	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7284	19987		1.51	1.4E-01	AW015373.1	EST_HUMAN	U1H-B10-aat-c-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7521	20192	33283	1.19	1.4E-01	U85945.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
7653	20317	33427	0.86	1.4E-01	AI305192.1	EST_HUMAN	q190b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8373	21066		1.23	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
8683	21375		0.57	1.4E-01	AK360893.1	EST_HUMAN	fr92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 002710 GAG POLYPROTEIN.
8811	21503	34650	4.18	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8892	21593	34722	0.59	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9021	21711	34864	0.97	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9021	21711	34865	0.97	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9085	21774	34938	8.81	1.4E-01	BF310659.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9175	21845	35011	1.24	1.4E-01	W69411.1	EST_HUMAN	z194a04.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
9246	21925	35095	0.46	1.4E-01	X73293.1	NT	M. variellii genes rpoH, rpoB and rpoA
9246	21926	35098	0.46	1.4E-01	X73293.1	NT	M. variellii genes rpoH, rpoB and rpoA
9258	21937	35111	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9258	21937	35112	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9350	20421	33541	1.93	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a (JAL), and zinc finger protein (DNZ1) genes, complete cds
9704	22355	35551	0.97	1.4E-01	X66092.1	NT	C. parvulus ORF for putative membrane transport protein
9887	22537	35732	1.26	1.4E-01	AF023813.1	NT	Macronitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
9888	22636	35846	0.56	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
9888	22636	35847	0.56	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22805	36022	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA
10157	22805	36023	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA
10360	23007		0.57	1.4E-01	T84293.1	EST_HUMAN	y47d03.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:111365 5'
10499	23145	36372	0.62	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
10607	23301		1.84	1.4E-01	AA1811480.1	EST_HUMAN	ac99a03.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
10746	23433	36676	3.24	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2N1b-Bst Homo sapiens cDNA clone IMAGE:154088 5'
10954	23631	36879	1.31	1.4E-01	AW104882.1	EST_HUMAN	xd73e10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11036	23707	36976	1.3	1.4E-01	T86102.1	EST_HUMAN	ye47g10.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120930 5'
11036	23707	36976	1.3	1.4E-01	T86102.1	EST_HUMAN	ye47g10.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120930 5'
11038	23709	36978	2.35	1.4E-01	P08948	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11262	23924	37215	1.68	1.4E-01	X68092.1	NT	C.perfringens ORF for putative membrane transport protein
11301	19867		1.41	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-eat-c-08-Q-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11446	23213	36445	2.37	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK),
11512	24112		1.82	1.4E-01	X52102.1	NT	triosephosphate isomerase (TPI) genes, complete cds
						NT	M.musculus p16K gene for 16 kDa protein
11743	24335	37661	1.83	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HBAR (HBar) gene, complete cds
11827	24411	37747	1.31	1.4E-01	AW684572.1	EST_HUMAN	h14h08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972319 3'
11827	24411	37748	1.31	1.4E-01	AW684572.1	EST_HUMAN	h14h08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972319 3'
12213	25172	30904	1.98	1.4E-01	AB000890.1	NT	Ephydratia fluviatilis mRNA for aldolase, partial cds
12261	24706	31049	2.03	1.4E-01	X74773.1	NT	P.salina plasmid gene secY
12276	24714		2.2	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
12318	25393		2.84	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12413	24794		1.35	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
12425	24801		2.97	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 2327, 2888767-3002865
12500	25407		3.15	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12708	25221		6.26	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
12778	25033		2.37	1.4E-01	AW377898.1	EST_HUMAN	MFR0-HT0208-221298-204-c08 HT0208 Homo sapiens cDNA
314	13118	25756	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
314	13118	25757	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
516	13300	25832	2.8	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
621	13400	26035	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
621	13400	26036	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
824	13594	26264	0.92	1.3E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
874	13643	26313	1.8	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1005	13765	26425	1.31	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1105	13862		2.6	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1193	13945	26809	1.13	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1425	14172		1.18	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein GMS mRNA, complete cds
1850	14588	27303	0.97	1.3E-01	6680857	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
1952	14687	27400	2.18	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2167	14896		1.22	1.3E-01	AJ243578.1	NT	Rhodospseudomonas actinophila puc85, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2288	15013		1.2	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-d12 ST0173 Homo sapiens cDNA
2379	15101		3.34	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	15308	28042	4.76	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3065	15831	28474	1.01	1.3E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3443	16188	28849	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3669	16718		1.43	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4117	16859		1.27	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4137	16879		4.24	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081289-036-e03 DT0018 Homo sapiens cDNA
4145	16887	29518	2.03	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4163	16903	29532	18.52	1.3E-01	AW273741.1	EST_HUMAN	x123810.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2813895 3'
4257	16998	29627	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4257	16998	29628	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4279	17018		12.76	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4445	17181	29806	0.77	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4497	17233	29863	2.68	1.3E-01	BE272339.1	EST_HUMAN	601126038F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2860063 5'
4863	17698		0.74	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA
5242	18048	30677	0.83	1.3E-01	AW468988.1	EST_HUMAN	ha07b06.x1 NCL_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5278	18083	30739	2.23	1.3E-01	AW804417.1	EST_HUMAN	L1 repetitive element ;
5414	18213		0.77	1.3E-01	AF107793.1	NT	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5497	18295		0.75	1.3E-01	AF056880.1	NT	Emizella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5638	18433	31346	0.97	1.3E-01	BF210920.1	EST_HUMAN	Hepatitis C virus 68_GL10 genome polyprotein gene, partial cds
5896	18681	31628	0.57	1.3E-01	BF527281.1	EST_HUMAN	601874591F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4101119 5'
5896	18681	31629	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6392	19161	32162	15.12	1.3E-01	AB031326.1	NT	602039337F2 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6474	19241	32241	1.95	1.3E-01	X88891.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6691	19608		0.75	1.3E-01	W26367.1	EST_HUMAN	C.jacchus intron 4 of visual pigment gene (red allele)
							2673 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6814	19651		0.99	1.3E-01	BF629560.1	EST_HUMAN	602044346F1 NCL_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4181868 5'
7162	19649		1.96	1.3E-01	H48884.1	EST_HUMAN	y33d02J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
7859	20554		0.88	1.3E-01	BE272339.1	EST_HUMAN	601126006F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
7873	20568	33694	1.34	1.3E-01	11423284	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
7802	20597	33727	1.17	1.3E-01	BF680622.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8136	20630		0.51	1.3E-01	BE562528.1	EST_HUMAN	601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8172	20666	33988	0.64	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8243	20637		4.47	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDLO54c
8285	20678		4.44	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8428	21119	34258	1.02	1.3E-01	BF680622.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8847	21538	34683	0.58	1.3E-01	R11172.1	EST_HUMAN	y69g11J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
8847	21538	34684	0.58	1.3E-01	R11172.1	EST_HUMAN	y69g11J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9119	21807	34973	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9119	21807	34974	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9372	21647	35120	3.71	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+-K+-ATPase alpha 2c subunit mRNA, complete cds
9671	22323		0.56	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
9851	22589		0.89	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10030	22678	35694	0.85	1.3E-01	AW851599.1	EST_HUMAN	MR2-CT0222-201098-001-a01 CT0222 Homo sapiens cDNA
10291	25128	36151	1.1	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10423	23069	36280	0.64	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10471	23117	36347	0.62	1.3E-01	AW247836.1	EST_HUMAN	2820637.3 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
10528	23225		2.93	1.3E-01	BF330699.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
10776	23458	36701	1.56	1.3E-01	H01883.1	EST_HUMAN	y62d09J1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150449 5'
11039	23710	36980	1.33	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11216	23879		3.28	1.3E-01	6871745	NT	Mus musculus cofilin 2, muscle (Cfil2), mRNA
11304	23963	37263	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11304	23963	37284	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11589	24188	37540	4.26	1.3E-01	BE279449.1	EST_HUMAN	601158032F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11723	24317	37604	1.94	1.3E-01	BE618364.1	EST_HUMAN	601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
11765	24346	37676	1.44	1.3E-01	BF683655.1	EST_HUMAN	602139760F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300863 5'
12114	24607	31088	1.37	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12247	24695		4.43	1.3E-01	AJ242790.1	NT	Gallus gallus sox1 gene for lymphodactin, exons 1-3
12274	24713		1.51	1.3E-01	Z13994.1	NT	R. norvegicus ctp2 gene for cystatin related protein 2
12806	24915		1.43	1.3E-01	AB026829.1	NT	Ephydra flumilis mRNA for sALK-6, complete cds
12836	24936		2.28	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Soares Dieckgraebe cdon_NHCD Homo sapiens cDNA clone IMAGE:2520877 3' similar to
374	13189	25844	8.42	1.2E-01	AK21744.1	EST_HUMAN	tf39b02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_ma1
415	12826		1.05	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
534	13317		4.33	1.2E-01	AF039442.1	NT	Dicystostellum discoideum ORF DG1016 gene, partial cds
1355	14103	26778	3.22	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	14103	26778	3.22	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1362	14110		4.36	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1496	14243		1.23	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdAAJB11 5'
1627	14373	27082	1.28	1.2E-01	Q14934	SWISSPROT	a48e09.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1646	14382	27082	2.81	1.2E-01	AI285402.1	EST_HUMAN	Q16671 ANTH-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ;
1762	14504		20.17	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR
1913	14650		1.03	1.2E-01	AW449368.1	EST_HUMAN	NFAT3) (NF-ATC4) (NF-AT3)
2181	14910	27642	1.75	1.2E-01	BF248480.1	EST_HUMAN	qf69f09.x1 NCI_CGAP_Eac2 Homo sapiens cDNA clone IMAGE:1880553 3'
2284	15009	27748	1.2	1.2E-01	AL163213.2	NT	H.sapiens DNA for endogenous retroviral like element
2597	15311	28047	1.49	1.2E-01	AW906556.1	EST_HUMAN	UI-H-B13-aid-e-10-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2731	15438	28176	1.12	1.2E-01	AI623388.1	EST_HUMAN	601821667F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2847	15615	28262	1.3	1.2E-01	U18018.1	NT	Homo sapiens chromosome 21 segment HS21C013
2803	15559	28318	2.5	1.2E-01	AI720470.1	EST_HUMAN	QV3-BND046-220300-123-f10 BND046 Homo sapiens cDNA
2835	15701	28350	2.92	1.2E-01	M16384.1	NT	ts18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
3004	15770	28418	0.97	1.2E-01	X56882.1	NT	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN, [1] ; contains element PTR5 repetitive
3224	15987	28641	1.89	1.2E-01	AW370668.1	EST_HUMAN	element ;
3252	16014		1.12	1.2E-01	U67800.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
3472	16228		0.8	1.2E-01	Z99118.1	NT	ss80c09.x1 Barstead cdon_HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
3511	16267	28921	0.82	1.2E-01	X56882.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
							Human creatine kinase-B mRNA, complete cds
							Human mRNA for a group 3 late embryogenesis abundant protein (LEA)
							QV1-BT0259-261089-021-c05 BT0259 Homo sapiens cDNA
							Methanococcus jannaschii section 142 of 150 of the complete genome
							Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
							Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3511	16257	28922	0.82	1.2E-01	X56982.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3592	16228		1.46	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
4160	16900	29528	1.97	1.2E-01	Z54255.1	NT	P.claridi mRNA; repeat region (ID 2MR17)
4160	16900	29528	1.97	1.2E-01	Z54255.1	NT	P.claridi mRNA; repeat region (ID 2MR17)
4672	17408	30041	1.1	1.2E-01	Z48163.1	NT	Lescurantum mRNA for glycylase-1
4739	17471		0.92	1.2E-01	AF221633.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5170	17979	30492	0.81	1.2E-01	AA744369.1	EST_HUMAN	ny63cd04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282850 3'
5217	18025	30849	1	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5227	18034	30859	2.59	1.2E-01	W33035.1	EST_HUMAN	z508d02.r1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5284	18089	30749	2.3	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5418	18217	30928	0.88	1.2E-01	Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6107	18884	31853	1.93	1.2E-01	BE620945.1	EST_HUMAN	601463518F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3895613 5'
6153	18930	31898	1.36	1.2E-01	P10942	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6208	18981	31980	2.35	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6270	19043	32020	1.54	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6337	19107	32097	0.57	1.2E-01	AA747535.1	EST_HUMAN	nd85cd01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6550	19315	32321	1.14	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4158388 5'
6700	19616	32658	0.59	1.2E-01	AF286739.1	NT	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7793	20498		1.4	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-280300-002-f09 BN0137 Homo sapiens cDNA
7882	20557	33683	4.38	1.2E-01	AI013753.1	EST_HUMAN	wc98g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
7908	20601	33731	0.87	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II;
8208	20902	34037	0.73	1.2E-01	AI032881.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CH-B22)
							at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
8295	20989		10.29	1.2E-01	AW083652.1	EST_HUMAN	xc49cd07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8315	21008		3.34	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8354	21047	34184	0.99	1.2E-01	J03956.1	NT	N.cressa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8354	21047	34185	0.99	1.2E-01	J03956.1	NT	N.cressa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8499	21191		1.09	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8589	21281		1.49	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8623	21315		0.82	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9471	22080	35252	2.83	1.2E-01	X77681.1	NT	S.cerevisiae HXT5 gene
8908	22555	35750	1.59	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
10811	23305	36543	1.38	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
10801	23484		2.17	1.2E-01	D28184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10989	23672		3.18	1.2E-01	BE882324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11084	23764		1.68	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11220	23883	37168	2.61	1.2E-01	AF180483.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNAI1) gene, exon 17
11283	23944	37238	1.65	1.2E-01	R40249.1	EST_HUMAN	y80c02.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11482	24093		1.67	1.2E-01	M65108.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11692	24462		2.53	1.2E-01	AV659033.1	EST_HUMAN	AV659033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12230	24683		3.52	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12305	25351	30605	2.87	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12417	24798		3.16	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12419	13317		3.19	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12525	24872		2.11	1.2E-01	X53381.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12586	25394	30611	1.44	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
12610	24917	31007	5.86	1.2E-01	AI289903.1	EST_HUMAN	qn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12632	24932		2.83	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12638	25289		7.95	1.2E-01	Q98433	SWISSPROT	CYCJUN T
12663	24982	30989	1.39	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 83 of the complete chromosome
12800	16228		1.91	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
12812	25372	30614	1.38	1.2E-01	9845282	NT	Mus musculus protein (16kDa) similar to human SYK interacting protein (p16K), mRNA
651	13334	25964	0.8	1.1E-01	AI561003.1	EST_HUMAN	h18d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167883 3'
601	13379	26010	1.65	1.1E-01	AA569008.1	EST_HUMAN	hmo08g11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb.X06985_jma1
1032	13792	28452	2.03	1.1E-01	BF607308.1	EST_HUMAN	H1EMV OXYGENASE 1 (HUMAN);
1063	13821		1.3	1.1E-01	AL161560.2	NT	602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1136	15561	26552	4.92	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, config fragment No. 60
1227	13977	26648	3.01	1.1E-01	D64004.1	NT	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1511	14257	26943	2.52	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, Z3127, 2898787-3002865
2312	15037		1.95	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
							Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2540	15530		1	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2572	15286		1.17	1.1E-01	AW821809.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3030	15798	28442	0.82	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3336	16096		1.76	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3415	16173	28822	2.11	1.1E-01	BE393188.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627068 5'
3444	16200	28850	1.21	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XX
3570	16325	28972	0.77	1.1E-01	Y07695.1	NT	A.limmerus gene for transposase
3688	16441		0.74	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3696	16450	29089	1.47	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4080	16833	29456	1.28	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0290 Homo sapiens cDNA
4080	16833	29457	1.28	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0290 Homo sapiens cDNA
4228	16967		8.78	1.1E-01	AF167068.1	NT	Drosophila melanogaster kismet protein (Mar) mRNA, complete cds
4254	16995	29624	0.77	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4594	17329	29956	0.96	1.1E-01	S44957.1	NT	Tapa-1=Integral membrane protein TAPA-1 [liver, B cell lymphoma line 39C13, Genomic, 1973 nt, segment 1 of 7]
4780	17512	30134	1.2	1.1E-01	Y07695.1	NT	A.limmerus gene for transposase
4957	16839		0.85	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PEX2, RAAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-PP, and tanascin X (TNX) genes, complete>
5077	17798	30412	1	1.1E-01	P70281	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
5584	18391		1.4	1.1E-01	AA747216.1	EST_HUMAN	rx78a03.s1 NC1_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5653	18448	31361	1.23	1.1E-01	AF020827.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5687	18490	31399	0.68	1.1E-01	AL110385.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5745	18537	31459	1.81	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5781	18572	31500	5.31	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
5936	18718	31676	1.67	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
5955	18737	31826	1.75	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
5976	18767	31719	9.4	1.1E-01	AW853698.1	EST_HUMAN	RC3-CT0264-280989-011-a01 CT0264 Homo sapiens cDNA
6330	19100	32088	0.67	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6338	19108	32098	1.25	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6381	19150	32149	0.72	1.1E-01	AF036707.1	EST_HUMAN	q976d08.x1 Sporea_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841089 3'
6512	19277	32278	3.71	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6604	19367		3.03	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6697	19614	32855	2.81	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6948	19430	32445	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
6948	19430	32446	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7087	25423		0.89	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4050653 5'
7203	25107	32884	0.84	1.1E-01	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1169001-1485000 nt, position (977)
7435	20112	33189	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7435	20112	33200	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7555	20225	33329	1.93	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7595	20283	33371	3.35	1.1E-01	AA788784.1	EST_HUMAN	ab31506.s1 Soares parathyroid tumor NIHHPA Homo sapiens cDNA clone 1240403 3' similar to gb-J03483
7868	20563	33690	0.5	1.1E-01	U67492.1	NT	CHROMOGHRANIN A PRECURSOR (HUMAN);
8107	20801	33933	1.7	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8107	20801	33934	1.7	1.1E-01	AA493574.1	EST_HUMAN	nr04gt10.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.15	1.1E-01	X81233.1	NT	nr04gt10.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8193	20887		1.14	1.1E-01	AW817818.1	EST_HUMAN	H. sapiens IL15 gene
8249	20943	34081	1.45	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-409 ST0270 Homo sapiens cDNA
8717	21409	34552	2.08	1.1E-01	U02482.1	NT	DKFZp547P194_1 547 (synonym: hifor1) Homo sapiens cDNA clone DKFZp547P194 5'
8810	21502	34649	0.88	1.1E-01	A1807474.1	EST_HUMAN	Pedococcus acidilactici H1 plasmid pSMB74 pectin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8906	21597	34739	0.47	1.1E-01	AF050081.1	NT	wf48c01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358818 3' similar to contains Alu repetitive element
8941	21632	34775	2.04	1.1E-01	AA182153.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
8941	21632	34776	2.04	1.1E-01	AA182153.1	EST_HUMAN	zp63b12.11 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:627743 5'
9033	21723	34877	0.74	1.1E-01	Y12727.1	NT	zp63b12.11 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:627743 5'
9063	21762	34912	2.04	1.1E-01	TT2876.1	EST_HUMAN	P. furiosus partial dph5 gene and argF gene
9090	21779		0.8	1.1E-01	BE983280.1	EST_HUMAN	yd18r03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9322	21989		0.88	1.1E-01	BE142305.1	EST_HUMAN	GM3-HT0142-27/1089-026-g11 HT0142 Homo sapiens cDNA
9366	22058		2	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
9810	22461		0.5	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10017	22865		0.45	1.1E-01	BE315509.1	EST_HUMAN	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
10106	22764		1.57	1.1E-01	R80580.1	EST_HUMAN	y99a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147084 3'
10235	22863	36098	1.26	1.1E-01	U60529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10708	15786	28442	2.05	1.1E-01	F03285.1	EST_HUMAN	HSC1RFO22 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10840	23622		2.76	1.1E-01	AF16032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
10974	23650	36903	3.91	1.1E-01	R23708.1	EST_HUMAN	YH5F12.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element/contains TAR1 repetitive element;
10983	23658	36911	1.39	1.1E-01	6981361	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (PFk), mRNA
11002	18480	31399	1.31	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11134	23802	37078	1.56	1.1E-01	X70058.1	NT	Mytilus edulis cytochrome gene
11169	23836	37117	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tg and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11169	23836	37118	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tg and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11277	23938	37230	2.81	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11874	24269		1.66	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
11890	24529		1.36	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12098	24598		3.92	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-403 NT0112 Homo sapiens cDNA
12341	25160		1.97	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
12750	25012	30977	3.15	1.1E-01	BF239763.1	EST_HUMAN	601808350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1179	13932		2.74	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1249	13936	26985	2.63	1.0E-01	AI985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.
1371	14119	26794	1.95	1.0E-01	AL161504.2	NT	MER7 repetitive element;
2493	15210	27952	1.11	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3503	16259	28913	1.19	1.0E-01	BF033991.1	EST_HUMAN	UI-H-B13-alc-4-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738420 3'
3708	16461	29100	1.03	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3859849 5'
3817	16569	29200	0.96	1.0E-01	AF297081.1	NT	601808489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3817	16569	29201	0.96	1.0E-01	AF297081.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3935	16885	29326	2.53	1.0E-01	BF365703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4518	17253		0.95	1.0E-01	AI792349.1	EST_HUMAN	QV2-NT0048-160800-318-e05 NT0048 Homo sapiens cDNA
4684	17398	30032	1.19	1.0E-01	U50450.1	NT	an32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4686	17594	30217	2.35	1.0E-01	AW952344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (fex) mRNA, complete cds
5238	18044		9.73	1.0E-01	W86490.1	EST_HUMAN	EST364414 IMAGE resequences, MAGB Homo sapiens cDNA
5789	18580		1.21	1.0E-01	AK024472.1	NT	zh62h04.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5934	18717	31675	14.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ000065 protein, partial cds
6243	19017	31961	0.99	1.0E-01	AA481878.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6258	19030	32005	0.7	1.0E-01	AA406039.1	EST_HUMAN	zu41g10.s1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.13 L1 repetitive element;
							zu67c12.s1 Soares_beside_NHT Homo sapiens cDNA clone IMAGE:743062 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6924	19680		1.81	1.0E-01	R23821.1	EST_HUMAN	y334108.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131676 6' similar to contains Alu repetitive element;
7635	20300		2.67	1.0E-01	Y12488.1	NT	M.musculus wtn gene
7709	20373	33486	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7709	20373	33487	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7834	20529	33656	0.65	1.0E-01	AA861091.1	EST_HUMAN	ak32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407686 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8066	20760		0.5	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8390	21083		0.98	1.0E-01	AW189797.1	EST_HUMAN	x09b01.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element ;
9084	21773	34937	1.04	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapman mRNA, complete cds
9395	22057	35228	0.51	1.0E-01	R44593.1	EST_HUMAN	y833104.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9407	22069		1.6	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9450	22000		3.02	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J59 section 62 of 132 of the complete genome
9464	22074	35245	0.75	1.0E-01	W01955.1	EST_HUMAN	zs68c10.s1 Soares_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:327282 3'
9721	22372	35571	1.67	1.0E-01	BF240154.1	EST_HUMAN	601805561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9835	22486	35687	8.12	1.0E-01	AB046789.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9835	22486	35688	8.12	1.0E-01	AB046789.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10043	22691		0.97	1.0E-01	AW957425.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
10048	22696	35912	0.51	1.0E-01	T51952.1	EST_HUMAN	y628a06.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72862 3' similar to contains Alu repetitive element
10228	22877	36089	0.89	1.0E-01	BE782750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939086 5'
10554	23250		1.95	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10958	23634	36884	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4106089 5'
10958	23634	36885	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11376	23983	37283	6.22	1.0E-01	BE780543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
11510	24110		1.52	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain-RIMD 0508952
11594	24193	37511	1.48	1.0E-01	Z71448.1	NT	A.thaliana mRNA for CLC-b chloride channel protein
11594	24193	37512	1.48	1.0E-01	Z71448.1	NT	A.thaliana mRNA for CLC-b chloride channel protein
11832	24416	37755	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
11832	24416	37756	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
12083	24921		4.32	1.0E-01	BE637719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451633 6'
12300	24725		1.71	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12317	24738		2.22	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
12614	24921		2.74	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12677	25318		5.03	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12733	25002		8.8	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2781	15486	28224	1.27	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R11) mRNA, complete cds
2780	15495	28235	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2780	15495	28236	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3260	16022	28871	1.32	9.9E-02	AF068810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
3633	16883	29324	0.75	9.9E-02	AI821637.1	EST_HUMAN	zu46003.x6 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740932 3'
4632	17367	30003	0.93	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278898 3'
6875	17951	30547	9.17	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
7815	20510	33834	0.83	9.9E-02	AW103086.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
7815	20510	33835	0.83	9.9E-02	AW103086.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
9158	21887	35055	0.98	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
550	13333		1.43	9.8E-02	X56338.1	NT	O. sativa RAm9C gene for alpha-amyrase
3100	15865		0.9	9.8E-02	4604578	NT	Homo sapiens I factor (complement) (IF) mRNA
3142	15906	28550	3.64	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4198	16939	29564	6.24	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4198	16939	29565	6.24	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7381	20061		0.77	9.8E-02	X54133.1	NT	Human HIP1 delta mRNA for protein tyrosine phosphatase delta
9153	21884		1.18	9.8E-02	M61843.1	NT	Human laminin B1 chain gene, exon 26
11437	23204	36436	2.05	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3864287 5'
12052	24570		1.78	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mept), mRNA
1328	14077	26752	1.31	9.7E-02	AB005808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds
1580	14326		1.49	9.7E-02	4603710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2257	14884	27724	2.08	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3965	16714		3.48	9.7E-02	Q98785	SWISSPROT	CELL_SURFACE_A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5261	18067	30685	0.94	9.7E-02	AF069189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5261	18087	30696	0.94	9.7E-02	AF089189.1	NT	Caulobacter crescentius thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5924	18708	31862	1.43	9.7E-02	AW954476.1	EST_HUMAN	EST366548 IMAGE resequences, MAGC Homo sapiens cDNA
7198	19894	32958	3.24	9.7E-02	Z89119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2897771 to 3213410
7882	20577	33705	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7882	20577	33706	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8748	21440	34587	1.49	9.7E-02	AI953884.1	EST_HUMAN	wk78b08.x1 NCI CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gbX62851_mel
11152	23819		2.84	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2009	14744	27470	1.11	9.6E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (Lgtin) mRNA, partial cds
2009	14744	27471	1.11	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4311	17050	29675	5.8	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4940	17668	30276	0.99	9.6E-02	AW668230.1	EST_HUMAN	Proteus mirabilis fibrinolytic operon, strain H14320
6014	17895		3.13	9.6E-02	BE910039.1	EST_HUMAN	EST378303 IMAGE resequences, MAGI Homo sapiens cDNA
8274	20988		0.6	9.6E-02	AU137084.1	EST_HUMAN	601488088FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
9444	22121	35300	1.31	9.6E-02	AV687898.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9772	22423		1.12	9.6E-02	BE894895.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAH02 5'
9839	22587	35790	1.29	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5'
9839	22587	35791	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10020	22668	35984	0.5	9.6E-02	BF677270.1	EST_HUMAN	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10051	22669	35915	1.54	9.6E-02	AB013985.1	NT	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10051	22669	35916	1.54	9.6E-02	AB013985.1	NT	Antitritinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10158	22806	36024	3.35	9.6E-02	P08174	SWISSPROT	Antitritinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10843	23334	36572	7.22	9.6E-02	Z79702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
12652	24954		3.34	9.6E-02	H14589.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome; segment 102162
4081	16825	29432	2.1	9.5E-02	AW982395.1	EST_HUMAN	ym18h03.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:48853 3'
5579	16376	31289	0.85	9.5E-02	P51854	SWISSPROT	CM2-BN0023-060200-087-f12 BN0023 Homo sapiens cDNA
6988	19681	32728	0.55	9.5E-02	AA780728.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7202	19888	32963	4.72	9.5E-02	AB003473.1	NT	ac68a09.s1 Stragene fetal refina 837202 Homo sapiens cDNA clone IMAGE:667736 3'
7467	20141	33234	7.68	9.5E-02	AL161536.2	NT	Trimeresurus flavoviridis DNA for phosphodiesterase A2 inhibitor, complete cds
7597	18376	31289	0.84	9.5E-02	P51854	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7780	20475	33600	1.83	9.6E-02	BF038861.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7780	20475	33601	1.83	9.6E-02	BF038861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10578	23273	36509	2.36	9.6E-02	BF038861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10578	23273	36510	2.38	9.5E-02	BF038861.1	EST_HUMAN	601453842F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857243 5'
1825	14584	27275	2.82	9.4E-02	BF071083.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291817 5'
1857	14585	27310	0.89	9.4E-02	U55944.1	NT	Canis porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1857	14585	27311	0.89	9.4E-02	U55944.1	NT	Canis porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3860	18810	28249	4.43	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
6225	18899	31976	0.83	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8498	21190		2.46	9.4E-02	Z46983.1	NT	Aerobacter sp. cysD, cobQ, cobM, lysS, rubA, rubB, estB, oxyR, ppk, mtrA, ORF2 and ORF3 genes
10851	20168	33288	2.44	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vcl genes, complete cds, and p135 gene, partial cds
11041	25255		1.76	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12871	24965		1.92	9.4E-02	AF180036.1	NT	Mycoplasma pulmonis hypothetical membrane protein P83 gene, complete cds
2888	15754		1.97	9.3E-02	4809280	NT	Homo sapiens BAH-associated protein 3 (BALAP3) mRNA
3026	15702		6.32	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NIESG1), mRNA
3251	16013	28685	1.85	9.3E-02	BF575511.1	EST_HUMAN	602133088F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4132	16874	28502	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4132	16874	28503	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4885	17419		2.04	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
5578	18373		0.87	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8148	20840	33972	0.82	9.3E-02	AW566007.1	EST_HUMAN	EST68 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9810	22263	35449	2.15	9.3E-02	BE962631.2	EST_HUMAN	601665988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10091	22739	35983	3.67	9.3E-02	Q16034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10091	22739	35954	3.67	9.3E-02	Q16034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10218	22856		3.5	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B11-afk-h-05-0-JL.s1 NCI_CGAP_Sub83 Homo sapiens cDNA clone IMAGE:2723553 3'
12184	25181		2.51	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12550	25209		8.43	9.3E-02	AW488150.1	EST_HUMAN	hd28h12x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
12752	25254		2.1	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bclg1 (BING1), tapasin (tapasin), RafGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), betat1, 3-galactosyl transferase (beta1,3-galactosyl tr>
222	13034	25688	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25689	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25670	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2224	14952		1.68	9.2E-02	R54156.1	EST_HUMAN	yg98h07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3175	15938	28587	3.28	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3289	16061	28709	0.85	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:926136 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3573	18328		1.28	9.2E-02	6755216	NT	Mus musculus pre T-cell antigen receptor alpha (Ptrna), mRNA
4213	18954		0.99	9.2E-02	U82048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4274	17013		0.78	9.2E-02	BE289722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2890176 5'
7907	20602	33732	1.98	9.2E-02	T49920.1	EST_HUMAN	y69c09.11 Stratagene placenta (#837225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:XB6009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8076	20770	33899	2.2	9.2E-02	X95255.1	NT	H. vulgare xylose isomerase gene
11695	24290	37614	1.27	9.2E-02	AF026652.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
12739	25412		1.4	9.2E-02	11488872	NT	Podospora anserina mitochondrion, complete genome
414	12825	25439	4.19	9.1E-02	X77895.1	NT	O. cuticulatus k12 keratin gene
4451	17187	29812	1.33	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 54
5843	18438	31352	1.44	9.1E-02	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G8d, G8e, G8f, BAT5, G5b, CSK2B, BATA, G4, Apo M, BAT3, BAT2, AIF-1, IC7, LST-1, LTB, TNF, and LTA genes, complete cds
7285	19968	33045	14.94	9.1E-02	AW180858.1	EST_HUMAN	au74605.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7575	20244	33349	0.78	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 47
7609	20275	33383	0.72	9.1E-02	U39073.1	NT	Mus musculus thymopolein zeta mRNA, complete cds
8822	21514	94659	0.88	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10327	22974		1.37	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
10354	23001	36218	1.25	9.1E-02	S74059.1	NT	Tg616=Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt]
10383	23029	36244	1.19	9.1E-02	Y11197.1	NT	A.thaliana RH1, TCI, G14587-5, G14587-8, and PRL1 genes
12110	25348		1.4	9.1E-02	AA179901.1	EST_HUMAN	zp38112.s1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12181	24653		2.12	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12637	25204		1.83	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
727	13501	26155	4.3	9.0E-02	P16328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1631	14377	27064	5.28	9.0E-02	BE220482.1	EST_HUMAN	h39970.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
2806	15511	26252	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2806	15511	28253	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3331	16091	28744	0.84	9.0E-02	AF278135.1	NT	Dichytellium discoidium spore coat structural protein SP65 (cotE) gene, complete cds
4619	17354	28989	3.27	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5906	18691	31640	5.21	9.0E-02	W58037.1	EST_HUMAN	z888d12.r1 Soares_fetal_lung_Nb2HIL19W Homo sapiens cDNA clone IMAGE:287694 5' similar to PIR:552171 S52171 small G protein - human ;
6819	19381		1.14	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Cor18 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;
6668	19585	32619	0.72	9.0E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HIL19W Homo sapiens cDNA clone IMAGE:138803 3'
12486	24945		2.01	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CsdD (csdD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1418	14168	26849	1.99	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285651 5'
1418	14168	26850	1.99	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285651 5'
2386	15107	27848	1.22	8.9E-02	BE153572.1	EST_HUMAN	PMD-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4175	16915		1.83	8.9E-02	AF286055.1	NT	Africanus angustatus AltranFla2 protein (AltranFla2) gene, partial cds
5760	18552	31474	3.22	8.9E-02	AW452122.1	EST_HUMAN	U1H-B13-alo-f-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088284 3'
5760	18552	31475	3.22	8.9E-02	AW452122.1	EST_HUMAN	U1H-B13-alo-f-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088284 3'
5776	18567	31498	3.39	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7093	19782	32848	1.64	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE]
7458	20132		2.06	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
7849	20644	33768	1.08	8.9E-02	P26476	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8030	20725	33858	0.72	8.9E-02	BF701685.1	EST_HUMAN	602128111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8030	20725	33859	0.72	8.9E-02	BF701685.1	EST_HUMAN	602128111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8496	21188	34331	4.72	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9520	22173	35356	0.8	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym16 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element;
9520	22173	35357	0.8	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym16 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element;
9892	22284	35477	0.76	8.9E-02	AA339396.1	EST_HUMAN	EST44454 Fetal brain I Homo sapiens cDNA 5' end
11882	25173		1.49	8.9E-02	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
11940	25207		1.48	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12085	24591		3.05	8.9E-02	BF696918.1	EST_HUMAN	602128682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12284	24716		1.61	8.9E-02	U28895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1352	14100	28775	1.59	8.9E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3883	18633	29272	1.03	8.9E-02	AA298128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4014	16760		3.55	8.8E-02	000288	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TF1D 135 KDA SUBUNIT (TAFII135) (TAFII130)
4214	16955		0.99	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4269	17009		1.27	8.8E-02	4590423	NT	Homo sapiens paired box gene 8 (aniridia, keratitis) (PAX8), isoform b, mRNA
7444	20120		0.57	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
8888	21577	34719	1.07	8.8E-02	AA151672.1	EST_HUMAN	zr98a05.s1 Stragene cdon (#837204) Homo sapiens cDNA clone IMAGE:566288 3'
11062	23732	37003	2.7	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11062	23732	37004	2.7	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11228	23891	37178	6.92	8.8E-02	AL040128.1	EST_HUMAN	DKFZp434D1313.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D1313 5'
11805	24395	37729	1.49	8.8E-02	P97803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155	24841	31098	2.66	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
1642	14388	27077	1.15	8.7E-02	A1167281.1	EST_HUMAN	ox65b01.s1 Soares_NIHMP-u_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3681	16434	29077	3.66	8.7E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3681	16434	29078	3.66	8.7E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4658	17392	30027	1.19	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5231	18037	30683	5.88	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5231	18037	30684	5.88	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6745	19578	32612	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6745	19578	32613	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6843	19426	32440	0.71	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
7761	20457		0.45	8.7E-02	AA284532.1	EST_HUMAN	z120e03.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:719892 3'
8413	21106	34245	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10610	23304		2.46	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' and
11282	23943	37237	2.55	8.7E-02	AJ007763.1	NT	Glucobacter oxydans RNA-1e and RNA-1a genes
12145	24693		2.1	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12340	24750		1.75	8.7E-02	6879057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1230	13979	26849	7.02	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2240	14908	27706	1.82	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3183	15946	28596	4.57	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3635	18388		3.77	8.6E-02	AF153392.1	NT	Dictyostellium discoideum adenyl cyclase (acrA) gene, complete cds
5134	17852		0.86	8.6E-02	BF570286.1	EST_HUMAN	602185716T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310289 3'
6003	18784	31746	4.75	8.6E-02	Y10828.1	NT	Homo sapiens LCN1b gene
6281	19054	32033	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6281	19054	32034	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7481	20153	33248	1.34	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (R-RELATED RECEPTOR)
7831	20526	33651	1.25	8.6E-02	5730068	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
7831	20526	33652	1.25	8.6E-02	5730068	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
7959	20664	33788	0.62	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8031	20726		0.81	8.6E-02	U60168.1	NT	Dictyostellium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9637	22289	35482	1.76	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jeggd2 gene, complete cds; and unknown gene
9673	22325		0.58	8.6E-02	AW662163.1	EST_HUMAN	h20c08.x1 NCI_CGAP_GU11 Homo sapiens cDNA clone IMAGE:2972846 3'
10063	22701	35918	0.81	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
10865	23545	36792	1.8	8.6E-02	AF206551.1	NT	Laccaria media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10865	23545	36793	1.8	8.6E-02	AF206551.1	NT	Laccaria media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11214	23877	37163	4.64	8.6E-02	BF305806.1	EST_HUMAN	601883437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11214	23877	37164	4.64	8.6E-02	BF305806.1	EST_HUMAN	601883437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11417	23184	38414	5.97	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11568	24187	37481	2.11	8.6E-02	AF283860.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2395	15116	27853	3.3	8.6E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5583	18380	31282	0.75	8.5E-02	AA985491.1	EST_HUMAN	cc83b07.s1 NCI_CGAP_Kd6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gb-K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5621	18417		1.29	8.5E-02	P06089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5921	18706	31658	6.95	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8504	21196	34340	1.65	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
9736	22387	35591	2.81	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
9736	22387	35592	2.81	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10261	22909	36119	0.54	8.5E-02	X76731.1	NT	V. armodytes gene for armodytoxin C
10382	23028	36243	0.87	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11105	23775		6.97	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11125	23794	37070	4.43	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12700	24981		3.8	8.5E-02	A362834.1	EST_HUMAN	EST172798 Ovary II Homo sapiens cDNA 5' end
2872	15602	28121	3.73	8.4E-02	W06330.1	EST_HUMAN	z444e11.1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:343532 5'
3801	16553	28184	1	8.4E-02	A1827586.1	EST_HUMAN	wf10f11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350221 3' similar to contains element MSR1 repetitive element;
4321	17060	28685	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4321	17060	28686	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5137	17855	30472	4.97	8.4E-02	AB042555.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
5229	18035	30661	9.84	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6590	18353	32368	1.72	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7928	20623	33751	7.18	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0790-250400-162-d05 BT0790 Homo sapiens cDNA
8741	21433	34578	1.01	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10260	22908	36118	1.83	8.4E-02	A1735184.1	EST_HUMAN	ss88g10.x1 Barstead cdon HPLR87 Homo sapiens cDNA clone IMAGE:2335942 3' similar to TR:O88312 O88312 GOB-4.;
12070	24584	31122	1.68	8.4E-02	R79408.1	EST_HUMAN	y83h12.1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2005	14741	27465	0.92	8.3E-02	5835680	NT	bodes hexagonus mitochondrion, complete genome
2005	14741	27468	0.92	8.3E-02	5835680	NT	bodes hexagonus mitochondrion, complete genome
3580	16335	28980	6.91	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3607	16360	29001	0.83	8.3E-02	A1436797.1	EST_HUMAN	fr82g08.x1 Scores_NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3607	16360	29002	0.83	8.3E-02	A1436797.1	EST_HUMAN	fr82g08.x1 Scores_NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6166	18943	31914	1.05	8.3E-02	A1942338.1	EST_HUMAN	w079f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
6273	19046	32023	3.05	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7880	20575	33702	2.98	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds
7911	20606		1.46	8.3E-02	AA865285.1	EST_HUMAN	og88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.11 L1.1
8198	20892		1.32	8.3E-02	AA987873.1	EST_HUMAN	og81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
9438	22116	35291	1.41	8.3E-02	AW583503.1	EST_HUMAN	io08h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;
9451	22001		1.88	8.3E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10240	22888		0.49	8.3E-02	AF020409.1	NT	Dicotyledon discoidium Doca (doca) mRNA, complete cds
12158	23353		1.67	8.3E-02	BE058458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928893 5'
1357	14105		7.15	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1481	14228	26914	1.88	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3071	15637		2.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3784	16536		1.35	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3989	16737	28371	1.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4251	16892	28617	4.97	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16892	28618	4.97	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16892	28619	4.97	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5022	17743	30354	2.44	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5070	17789		2.39	8.2E-02	Z69883.1	NT	T.inflatum transposon Resless DNA
5252	18058	30687	1.49	8.2E-02	BE897030.1	EST_HUMAN	601436576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6925	18661	32707	3.09	8.2E-02	AF305553.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7632	20298		0.57	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8670	21382	34509	2.95	8.2E-02	AW876128.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
9499	22182	35332	5.36	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9683	22315	35512	2.24	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
12164	24646	31102	4.03	8.2E-02	AE002248.2	NT	Chlamydia pneumoniae AF389, section 73 of 94 of the complete genome
12554	25138		3.65	8.2E-02	AF275398.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5688	18463	31378	0.79	8.1E-02	AE004008.1	NT	Xylella fastidiosa, section 152 of 228 of the complete genome
6286	18059	32040	1.19	8.1E-02	T11532.1	EST_HUMAN	A1494F Heart Homo sapiens cDNA clone A1494
7097	19786		0.86	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7482	20154		1.25	8.1E-02	AI692881.1	EST_HUMAN	wd86f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8238	20932	34067	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8238	20932	34068	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
9812	22463		1.84	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
11482	24083	37395	2.08	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	15534	25447	5.03	8.0E-02	AW954653.1	EST_HUMAN	EST368723 IMAGE resequences, MAGC Homo sapiens cDNA
915	13682	26344	0.78	8.0E-02	U60315.1	NT	Mollusca contagiosum virus subtype 1, complete genome
1694	15576	27134	9.95	8.0E-02	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1694	15576	27135	9.85	8.0E-02	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1898	14633	27343	3.27	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-B08 BT0347 Homo sapiens cDNA
2374	15086	27835	1.08	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17727, 2137259-2287259
2374	15086	27836	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17727, 2137259-2287259
2473	15181		4.2	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2823	13827	28498	0.98	8.0E-02	M23449.1	NT	Dictyostelium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2901	15667	28315	1.45	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3787	16549	28182	1.01	8.0E-02	AW988118.1	EST_HUMAN	EST378181 IMAGE resequences, MAGI Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4725	17457	30083	1.43	8.0E-02	AI434202.1	EST_HUMAN	131g02x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4764	17496		6.33	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5108	17826	30443	0.87	8.0E-02	AW207037.1	EST_HUMAN	U1-H-B11-afid-f-10-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721547 3'
5801	18591	31516	3.15	8.0E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7080	18591	31516	1.82	8.0E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8027	20722	33854	3.79	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9289	21856	35127	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9289	21856	35128	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10058	22706		0.55	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10692	23383	36823	2.27	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12185	24665	31070	6.39	8.0E-02	AJ005375.1	NT	Drosophila orena hunchback region
12748	17803		2.21	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2171	14900	27634	3.52	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
2978	15744	28392	7.26	7.9E-02	AI682029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2179846 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
3777	16529	29168	0.97	7.9E-02	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 88 (HSP88), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (qrt), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3832	16583	29217	5.01	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3832	16583	29218	5.01	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4845	17379	30011	0.89	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4155401 5'
4760	17492		1.31	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4851	17581	30204	1.02	7.9E-02	L24757.1	NT	Human bone sialoprotein (BNSP) gene, exons 2, 3 and 4
6597	19360		1.16	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-411 GN0042 Homo sapiens cDNA
7931	20626	33754	2.79	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smf4p (SMF4) gene, complete cds
9827	22575	35773	4.21	7.9E-02	AI081844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2 CE08811;
9827	22575	35774	4.21	7.9E-02	AI081844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2 CE08811;
1188	13940	28804	1.77	7.9E-02	AI783275.1	EST_HUMAN	ou56a02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;
1188	13940	28805	1.77	7.9E-02	AI793275.1	EST_HUMAN	ou56a02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression- Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5027	16484		2.47	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859693 5'
6976	19457	32479	0.88	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6976	19457	32480	0.88	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8684	21378	34520	0.71	7.8E-02	BE897847.1	EST_HUMAN	601440438F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8779	21471	34616	0.66	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
8951	21642	34789	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FVE-DSP1b mRNA, complete cds
8951	21642	34790	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FVE-DSP1b mRNA, complete cds
9261	22015	35183	1.07	7.8E-02	AA469354.1	EST_HUMAN	nc88b06.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
9701	22352	35547	0.62	7.8E-02	Z89124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3989281 to 4214814
10562	22358	36484	4.56	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12754	25015		3.82	7.8E-02	AF096349.1	NT	HIV-1 strain 97USNG30 from USA, envelope glycoprotein (env) gene, partial cds
1978	15598	28800	1.25	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3574	18328		1.87	7.7E-02	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5456	18255	31145	0.59	7.7E-02	AF082838.1	NT	Calus gallus collagen type XI alpha-1 (COL12A1) gene, promoter region and partial cds
7809	20504	33825	5.37	7.7E-02	AA402948.1	EST_HUMAN	zu53d11.1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPICEOSOME ASSOCIATED PROTEIN. ;
9735	22386	35580	3.94	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR056C
10031	22679	35995	0.85	7.7E-02	A1318662.1	EST_HUMAN	t80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28878 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10031	22679	35996	0.85	7.7E-02	A1318662.1	EST_HUMAN	t80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28878 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10933	23613	36883	4.51	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12389	25215		2.68	7.7E-02	11439859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3382	16141	28768	1.97	7.6E-02	BE514432.1	EST_HUMAN	601318425F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3403	16161	28812	1.14	7.6E-02	AA236447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3547	16302	28952	0.71	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6068	18787	31749	0.81	7.6E-02	A1061275.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6263	19037	32012	0.92	7.6E-02	BE378328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9270	22024	35194	1.47	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9797	22448		1.63	7.6E-02	AL136078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
10119	22767	35979	0.49	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
10247	22895		0.75	7.6E-02	BE959638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639810 3'
10487	23133	36359	0.71	7.6E-02	X82656.1	NT	Lesculentum mRNA for triose phosphate translocator
10487	23133	36360	0.71	7.6E-02	X82656.1	NT	Lesculentum mRNA for triose phosphate translocator
11678	24273	37595	2.45	7.6E-02	AW996845.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
767	13540	26189	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	13540	26200	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4472	17207	29833	1.17	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5762	18553	31477	0.91	7.5E-02	A1948714.1	EST_HUMAN	wq24h09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8236	20930	34066	1.05	7.5E-02	A1884367.1	EST_HUMAN	w152b02.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA
8405	21098	34234	1.17	7.5E-02	AU116913.1	EST_HUMAN	ENOLASE (HUMAN);
							AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
9932	22580		0.64	7.6E-02	BF221730.1	EST_HUMAN	7d61cd5.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10390	23036	36252	0.7	7.5E-02	BF206809.1	EST_HUMAN	MER27 repetitive element;
10488	23134	36361	0.72	7.5E-02	X79460.1	NT	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
465	13260	25891	1.46	7.4E-02	AW838547.1	EST_HUMAN	C.fiml DSM 20113 16S rDNA
1445	14192		0.92	7.4E-02	AF030027.1	NT	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
2585	16299		1.32	7.4E-02	6755089	NT	Equine herpesvirus 4 strain NS80567, complete genome
3581	16336	28981	0.86	7.4E-02	A1807885.1	EST_HUMAN	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
4656	17390	30024	2.03	7.4E-02	L78810.1	NT	wf43h01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4741	17473	30108	2.94	7.4E-02	6878442	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4889	17616	30235	2.1	7.4E-02	6678462	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
6403	19172		2.18	7.4E-02	R17477.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
7801	20498	33618	1.52	7.4E-02	BE880112.1	EST_HUMAN	y914g06.r1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
8399	21092	34228	1.03	7.4E-02	U56089.1	NT	601493360F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
							Human perlecanin protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9064	21753	34913	1.12	7.4E-02	AW629605.1	EST_HUMAN	h167d11.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9064	21763	34914	1.12	7.4E-02	AW628605.1	EST_HUMAN	h167d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9339	20410	33525	0.52	7.4E-02	A1672839.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9339	20410	33526	0.52	7.4E-02	A1672839.1	EST_HUMAN	we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9714	22365	35563	1.03	7.4E-02	U62233.1	NT	we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9841	22492	35692	0.52	7.4E-02	BF512678.1	EST_HUMAN	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10339	23619	36869	1.28	7.4E-02	AA059187.1	EST_HUMAN	UI-H-BW1-ang-g-06-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3068898 3'
12126	24618		1.53	7.4E-02	11525893	NT	zf64e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
12381	25329		2.21	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-8), mRNA
468	13242	25881	1.5	7.3E-02	BE94961.2	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
458	13242	25882	1.5	7.3E-02	BE94961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
669	13445	26085	3.9	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1464	15570	26900	3.62	7.3E-02	AW900281.1	EST_HUMAN	Thermotoga maritima section 101 of 136 of the complete genome
1837	15580		12.41	7.3E-02	AL163302.2	NT	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
6361	19131	32126	1.32	7.3E-02	AA778977.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
7368	20048	33128	2.68	7.3E-02	P05149	SWISSPROT	z24e02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7368	20048	33129	2.58	7.3E-02	P05143	SWISSPROT	gbL02426 26S PROTEASE SUBUNIT 4 (HUMAN);
8068	20782		1.15	7.3E-02	7682107	NT	PROLINE-RICH PROTEIN MP-3
9110	21798		1.14	7.3E-02	AB011090.1	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
11179	19131	32128	2.06	7.3E-02	AA778977.1	EST_HUMAN	Homo sapiens mRNA for KIAA0518 protein, partial cds
11844	24428		5.07	7.3E-02	11560139	NT	z24e02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
117	12837	25577	1	7.2E-02	AE000882.1	NT	gbL02426 26S PROTEASE SUBUNIT 4 (HUMAN);
117	12837	25578	1	7.2E-02	AE000882.1	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC84171), mRNA
1458	14205	26890	2.72	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1028155 to 1039834 (section 88 of 148) of the complete genome
1458	14205	26891	2.72	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1028155 to 1039834 (section 88 of 148) of the complete genome
2552	15267		2.83	7.2E-02	U14794.1	NT	Homo sapiens chromosome 21 segment HS21C101
3865	16615	29254	0.95	7.2E-02	AW298322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
4312	17051	29678	4.65	7.2E-02	BF572307.1	EST_HUMAN	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
4644	17378	30010	0.7	7.2E-02	11466563	NT	UI-H-BW0-aj-e-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2792049 3'
							602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
							Rhodospirillum rubrum complete genome

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5205	18013	30635	2.88	7.2E-02	U07531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5206	18014	30636	10.1	7.2E-02	P11120	SWISSPROT	CALMODULIN
7068	19759	32824	1.58	7.2E-02	BF216088.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085710 5'
7085	19775	32840	0.64	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7109	19797		1.5	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8087	20781	33910	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8087	20781	33911	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8902	21653		0.61	7.2E-02	Y17217.1	NT	Lactococcus lactis capsE gene
9474	22127		0.49	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9511	22184	35348	2.32	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DGA Homo sapiens cDNA clone DCAAUG01 5'
9858	22311	35509	3.8	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9814	22465	35667	0.93	7.2E-02	BF126389.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028438 5'
9903	22552	35747	2.53	7.2E-02	AW873187.1	EST_HUMAN	h424f11.x1 NCI_QGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340
10082	22740	35955	0.62	7.2E-02	AA768204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
				7.2E-02	AA768204.1	EST_HUMAN	os62c07.s1 NCI_QGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10250	22898	36108	1.93	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10372	23018	36234	6.54	7.2E-02	BE865003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10395	23041		3.68	7.2E-02	BE539214.1	EST_HUMAN	601066194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451569 5'
10509	23155	36381	0.48	7.2E-02	AA706897.1	EST_HUMAN	z28h05.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
10830	23512	36753	3.3	7.2E-02	AF048874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11849	24433	37775	1.34	7.2E-02	AY009080.1	NT	Homo sapiens putative transmembrane protein decilin-1 mRNA, complete cds
12035	24560	31113	1.57	7.2E-02	AA773696.1	EST_HUMAN	af81a04.f1 Soares_NIH-IMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12069	24583		4.45	7.2E-02	AJ230786.1	EST_HUMAN	AJ230786 Homo sapiens library (Seranid P) Homo sapiens cDNA clone PS13D5 3'
12182	24654		1.73	7.2E-02	U82628.1	NT	Homo sapiens alodia telangiectasia (ATM) gene, complete cds
12196	25185		8.19	7.2E-02	AW900962.1	EST_HUMAN	OM4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
12599	25362		3.62	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
1897	14634	27344	2.01	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2290	15015	27751	5.07	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4092881 5'
7807	20502	33622	0.77	7.1E-02	A1125284.1	EST_HUMAN	qd52a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11922	24483		6.41	7.1E-02	BE304764.1	EST_HUMAN	607143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
515	13289	25831	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1486	14233		1.27	7.0E-02	X36377.1	NT	Martellia Mitcut-1 gene
1766	14498	27199	1.08	7.0E-02	AA056343.1	EST_HUMAN	z16804.s1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:506669 3'
3027	15793	28440	2.1	7.0E-02	AW138152.1	EST_HUMAN	UH-HB11-acy-c-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
							af65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K03002 60S
3878	16828	28288	0.74	7.0E-02	AA815438.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4118	16861		1.28	7.0E-02	AW782862.1	EST_HUMAN	C40-UJ0001-080300-270-612 UM0001 Homo sapiens cDNA
4189	16930	28560	1.06	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4877	17604	30227	7.24	7.0E-02	BF381887.1	EST_HUMAN	60718231F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
5283	18098		0.57	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7300	18983	33059	1.28	7.0E-02	AV689285.1	EST_HUMAN	AV689285 GK6 Homo sapiens cDNA clone GKCAE06 5'
7508	20177	33271	0.84	7.0E-02	Y10187.1	NT	Gallus gallus mRNA for partial ezrin, XL spliced variant (ecz gene)
8998	21698	34836	1.28	7.0E-02	8628113	NT	African swine fever virus, complete genome
9497	22150	35331	1.24	7.0E-02	K02801.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
9852	22502	35702	0.51	7.0E-02	U27388.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
11345	24035	37338	4.98	7.0E-02	AA724295.1	EST_HUMAN	ah88a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
501	13285	25917	4.3	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
501	13285	25918	4.3	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
						NT	Homo sapiens chromosome 21 segment HS21C010
1310	14058		1.2	6.9E-02	4507868	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3773	16525	28163	1.41	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3773	16525	28164	1.41	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucoside specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
5113	17831	30448	0.89	6.9E-02	AF121254.1	NT	607182383F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536253 5'
5127	17845	30462	1.25	6.9E-02	BE264605.1	EST_HUMAN	Canine distemper virus strain A7517, complete genome
7518	20187		0.61	6.9E-02	AF164987.1	NT	Human calmodulin (CALMT) gene, exons 2,3,4,5 and 6, and complete cds
7851	20846		1.12	6.9E-02	U12022.1	NT	6071340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8451	21143	34282	1.01	6.9E-02	BE567435.1	EST_HUMAN	6071340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8451	21143	34283	1.01	6.9E-02	BE567435.1	EST_HUMAN	Barbican duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
8018	21708	34860	0.7	6.9E-02	U22867.1	NT	X. laevis XFD2 mRNA for fork head protein
12065	24590		1.82	6.9E-02	X74315.1	NT	

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12232	24685		1.69	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFCHOMOLOG
12447	24817		1.46	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1875	14613	27321	1.56	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1875	14613	27322	1.56	6.8E-02	AA496759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1900	14637	27346	3.77	6.8E-02	AF156673.1	NT	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
3097	15882	28503	1.19	6.8E-02	AA781896.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3097	15882	28504	1.19	6.8E-02	AA781896.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
3097	15882	28505	1.19	6.8E-02	AA781896.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4516	17251		0.86	6.8E-02	BE141076.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBCSR14) gene, complete cds
6525	19291		0.6	6.8E-02	P20792	SWISSPROT	al75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376628 3'
6789	19460		1.09	6.8E-02	BE061890.1	EST_HUMAN	al75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376628 3'
7180	19896	32839	8.73	6.8E-02	AL163268.2	NT	al75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376628 3'
7584	20262	33358	0.63	6.8E-02	U16856.1	NT	al75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376628 3'
8186	20880	34017	5.01	6.8E-02	AJ248287.1	NT	MRO-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
8186	20880	34018	5.01	6.8E-02	AJ248287.1	NT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
11873	25379		2.3	6.8E-02	T03214.1	EST_HUMAN	RC1-BT0254-090300-017-c09 BT0254 Homo sapiens cDNA
12001	24537		2.85	6.8E-02	AA768014.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
12551	24898		1.65	6.8E-02	AW975839.1	EST_HUMAN	Dictyostelium discoideum myosin heavy chain kinase A (MHCK A) mRNA, complete cds
12613	24920		3.06	6.8E-02	9910585	NT	Pyrococcus abyssi complete genome; segment 5/6
1519	14266		1.93	6.7E-02	AF115536.1	NT	Pyrococcus abyssi complete genome; segment 5/6
1888	14623	27333	2.27	6.7E-02	AI220285.1	EST_HUMAN	FB4A8 Fetal brain, Stratiogene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
3708	18459	28097	4.92	6.7E-02	P12728	SWISSPROT	af67805.s1 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
7749	20445	33567	0.55	6.7E-02	X62895.1	NT	EST387948 IMAGE resequences, MAGN Homo sapiens cDNA
7749	20445	33568	0.55	6.7E-02	X62895.1	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
8337	21030	34167	0.47	6.7E-02	AW082688.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP101 allele, complete cds
9500	22153	35333	0.69	6.7E-02	AW137359.1	EST_HUMAN	qg79e04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
9500	22153	35334	0.69	6.7E-02	AW137359.1	EST_HUMAN	HOMEOBOX PROTEIN HOXD-4 (HOXA-4)
1948	14096	26771	1.07	6.6E-02	AF245116.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
2180	14909	27641	3.31	6.6E-02	AJ289241.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
3456	16212	28805	10.57	6.6E-02	RG4306.1	EST_HUMAN	xb67c11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
3471	16227	28881	2.59	6.6E-02	7108357	NT	U1-HB1-act-g-01-0-J1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
3471	16227	28882	2.59	6.6E-02	7108357	NT	U1-HB1-act-g-01-0-J1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
							Drosophila melanogaster cactin mRNA, complete cds
							Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
							y18b10.s1 Soares placenta N621P Homo sapiens cDNA clone IMAGE:195579 3'
							Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
							Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA

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4060	16805	28436	1.28	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4821	17649	30261	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4921	17649	30262	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6489	19256	32258	3.44	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6701	19283	32286	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6701	19283	32287	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7847	20542	33670	1.81	6.6E-02	AF032572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8372	21065	34206	0.84	6.6E-02	AF03055.1	NT	Dictyostellium discoideum darlin (dar) gene, complete cds
8678	21370		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8818	21511	34654	0.38	6.6E-02		NT	Human respiratory syncytial virus, complete genome
8819	21511	34655	0.38	6.6E-02	8629198	NT	Human respiratory syncytial virus, complete genome
8851	22501	35701	0.65	6.6E-02	A1458752.1	EST_HUMAN	697908.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2140488 3'
8887	22635	35845	1.66	6.6E-02	Y07648.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
10022	22670		0.83	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10883	23563	36811	0.88	6.6E-02	BF374248.1	EST_HUMAN	MF1-SN0064-010600-008-412 SN0064 Homo sapiens cDNA
11887	24461	37783	1.46	6.6E-02	AF032572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
12442	24812		2.66	6.6E-02	8937891	NT	Mus musculus DIPB gene (Dipb), mRNA
12740	25006		1.38	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
568	13349	25977	2.49	6.6E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3854178 5'
968	13732	26398	1.32	6.6E-02	7706088	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1370	14118	26783	3.08	6.6E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1728	14470	27169	1.77	6.6E-02	AE000794.1	NT	Aquifex aeolicus section 86 of 109 of the complete genome
6471	18270	31162	2.03	6.6E-02	AA443991.1	EST_HUMAN	z46h12.s1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6877	17953	30549	0.95	6.6E-02	U22661.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
8042	22493	35893	0.55	6.6E-02	BE983200.2	EST_HUMAN	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
8842	22493	35894	0.55	6.6E-02	BE983200.2	EST_HUMAN	601658817R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3855637 3'
10363	23010	36225	0.48	6.6E-02	BF106300.1	EST_HUMAN	601658817R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3855637 3'
10835	23232	36466	5.56	6.6E-02	AA195948.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11894	24403		3.73	6.6E-02	M21496.1	NT	z32g05.s1 Soares NIH-MIPu S1 Homo sapiens cDNA clone IMAGE:665144 3'
12240	24691		4.66	6.6E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
561	13343	25870	2.09	6.4E-02	X94549.1	NT	Nectria haematococca kinasin related protein 2 (KRP2) gene, complete cds
3014	15780	28429	0.96	6.4E-02	6996923	NT	A.cartae precursor of perlecan-chlorophylla-protein (PCP) gene
4839	15780	28429	1.18	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA

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5363	18165	30850	1.67	6.4E-02	AI191856.1	EST_HUMAN	q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR&Lb3 LTR8 repetitive element:
5791	18582	31509	0.65	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6022	18802	31783	4.21	6.4E-02	AF062733.1	NT	Heterodera glycines beta-1, 4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6022	18802	31784	4.21	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1, 4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6308	19080	32065	0.62	6.4E-02	AI672898.1	EST_HUMAN	we73g12.x1 Soares_Deckgrease_cotton_NHCD Homo sapiens cDNA clone IMAGE:2346760 3'
6719	19634	32677	6.43	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3650503 3'
7360	20041	33119	0.64	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 8/7
8234	20928		2.91	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
8563	21255	34392	3.42	6.4E-02	AA093305.1	EST_HUMAN	K1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9025	21715	34868	0.77	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Homo sapiens mRNA from cd24+ stem cells Homo sapiens cDNA clone CBDAIA10
9488	22139		0.55	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g08 OT0083 Homo sapiens cDNA
9617	22270	35457	1.73	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10161	22809	36027	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10161	22809	36028	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11709	24304	37628	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPTS) gene, complete cds
11709	24304	37630	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPTS) gene, complete cds
12141	25288		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12188	24659	31065	2.47	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1749	14491	27191	2.57	6.3E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; snRNP, G7A, NG23, MafS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
3580	16344		2.38	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6045	18825	31786	1.18	6.3E-02	BF210736.1	EST_HUMAN	6018733316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7142	18829		0.82	6.3E-02	X97889.1	NT	H. sapiens gene encoding La autoantigen
9191	21861	35028	1.04	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominica gene, exons 1-3
9913	22562	35758	2.64	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10171	22819		0.85	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10615	18825	31786	2.98	6.3E-02	BF210736.1	EST_HUMAN	6018733316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
4224	16965	29590	2.81	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4304	17043		1.02	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4542	17277		8.31	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)) (RO52)
6898	19815	32658	0.65	6.2E-02	D49830.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7527	20198	33282	1.03	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8846	25428		0.6	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
8243	21822	35082	0.52	6.2E-02	AA778450.1	EST_HUMAN	af20a08.s1 Soares total_fetus_Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1032178 3'
9380	22042	35214	1.65	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdf2), mRNA
11085	23765	37039	1.56	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11320	24011	37315	1.53	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chyl gene)
11865	24449	37791	1.74	6.2E-02	AF200359.1	NT	Rattus norvegicus UDP-glucose glycoprotein:glucosyltransferase precursor (Uggt) mRNA, complete cds
11989	25405		13.39	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12394	24782	31037	2.5	6.2E-02	BF112039.1	EST_HUMAN	TR-Q8Y4S8 Q8Y4S8 HYPOTHETICAL 30.3 KD PROTEIN. [1];
249	13058	25697	5.59	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3972	16721		2.28	6.1E-02	U73325.1	NT	Arabidopsis thaliana K ⁺ inward rectifying channel protein (AKG1) gene, complete cds
6023	18803		1.4	6.1E-02	4507070	NT	Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8161	20855	33988	3.75	6.1E-02	X92288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8559	21251	34388	0.57	6.1E-02	BE971853.1	EST_HUMAN	607651086R1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:3934604 3'
8559	21251	34389	0.57	6.1E-02	BE971853.1	EST_HUMAN	607651086R1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:3934604 3'
10830	23323	36560	4.91	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C08 HT0618 Homo sapiens cDNA
11862	24446	37787	1.27	6.1E-02	AB025333.1	NT	Epitetrus burgeri mRNA for RNA polymerase III largest subunit, partial cds
11945	25323		2.27	6.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
12633	24933		5.91	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
86	12922	25559	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.J1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:626310 5'
86	12922	25560	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.J1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:626310 5'
1239	13998	26855	1.54	6.0E-02	AE001777.1	NT	Thermococcus maritima section 89 of 136 of the complete genome
2082	15391	28130	1.09	6.0E-02	AW968848.1	EST_HUMAN	EST380824 MAGE resequences, MAGJ Homo sapiens cDNA
							Mesocricetus cori mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2775	15480		1.62	6.0E-02	AB031289.1	NT	
2837	12922	25559	0.8	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.J1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:626310 5'
2837	12922	25560	0.9	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.J1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:626310 5'

Table 4.

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3223	15886	28639	1.48	6.0E-02	AA372378.1	EST_HUMAN	EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3223	15886	28640	1.48	6.0E-02	AA372378.1	EST_HUMAN	EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3625	16378		0.72	6.0E-02	BE984443.2	EST_HUMAN	601688150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876080 3'
5037	17756	30370	0.69	6.0E-02	AF146738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5313	18117		0.94	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-01189-013-504 BT0253 Homo sapiens cDNA
6122	18900	31898	0.77	6.0E-02	AI807637.1	EST_HUMAN	wf48r05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 repetitive element;
6891	17887	30524	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6891	17887	30525	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7088	19777	32842	2.33	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4049228 5'
7580	20249	33355	2.13	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764188 3'
8321	21014		0.54	6.0E-02	11466495	NT	Recitomonas americana mitochondrion, complete genome
9172	21842	35007	1.17	6.0E-02	AI623167.1	EST_HUMAN	ls78a06.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9172	21842	35008	1.17	6.0E-02	AI623167.1	EST_HUMAN	ls78a06.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9308	21973	35147	1.68	6.0E-02	AJ245385.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9308	21973	35148	1.66	6.0E-02	AJ245385.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9805	22456	35659	0.5	6.0E-02	AA309787.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
9805	22456	35660	0.5	6.0E-02	AA309787.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11306	23965		1.89	6.0E-02	AA128388.1	EST_HUMAN	zn87c08.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:585166 5' similar to gb-x89181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
12187	24658	31064	2.19	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12564	24894		2.31	6.0E-02	AI809273.1	EST_HUMAN	wf88r03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:060288
223	13035	26671	3.87	6.0E-02	AW934719.1	EST_HUMAN	O60288 KIAA0551 PROTEIN;
2882	15748	28398	2.89	6.0E-02	AF160289.1	NT	RC1-DT0001-280100-012-010 DT0001 Homo sapiens cDNA
4817	17548	30173	1	5.9E-02	AF063304.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5123	17841	30457	0.73	5.9E-02	AW028748.1	EST_HUMAN	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
5123	17841	30458	0.73	5.9E-02	AW028748.1	EST_HUMAN	wf34e02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:065386
8515	21207	34350	1.88	5.9E-02	9055249	NT	O65386 F12F1.20 PROTEIN;
9351	20422		0.8	5.9E-02	BF242748.1	EST_HUMAN	wf34e02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:065386
							Mus musculus trophoblast related homeobox 5 (Drosophila) (hrx5), mRNA
							60187609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105894 5'

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23378		3.2	5.8E-02	6879870	NT	Mus musculus follistatin-like (Fstl), mRNA
10844	23623	36872	1.44	5.8E-02	11433356	NT	Homo sapiens ninein (LOC51198), mRNA
11544	24144		1.59	5.8E-02	AJ240733.1	NT	Gallus gallus HKO9 telomere junction
912	13879		5.18	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2884	15632		0.98	5.8E-02	AJ223821.1	NT	Populus trichocarpa GCoADMT1 gene, exon 1 to exon 5
4322	17081	29687	4.9	5.8E-02	AW051827.1	EST_HUMAN	wx24c02.x1 NCI CGAP Kld11 Homo sapiens cDNA clone IMAGE:2544578 3'
4322	17081	29688	4.9	5.8E-02	AW051827.1	EST_HUMAN	wx24c02.x1 NCI CGAP Kld11 Homo sapiens cDNA clone IMAGE:2544578 3'
4510	17245	29879	4.95	5.8E-02	AI247505.1	EST_HUMAN	q158f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR_X1 PRECURSOR (HUMAN);
4510	17245	29880	4.95	5.8E-02	AI247505.1	EST_HUMAN	q158f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR_X1 PRECURSOR (HUMAN);
4535	17270		2.62	5.8E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7578	20247	33362	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7578	20247	33353	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8565	21257	34394	0.67	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12084	24560		1.79	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12373	25396		7.06	5.8E-02	AA04289.1	EST_HUMAN	no75e11.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3053	15819	28463	1.38	5.7E-02	AI081844.1	EST_HUMAN	ou63b05.s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3068	15834	28476	1.28	5.7E-02	AF119117.1	NT	CE08611;
3694	16448		0.97	5.7E-02	AF001292.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3783	16535	29173	2.45	5.7E-02	AW966791.1	EST_HUMAN	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XI (ctt-12) and globin XI (ctt-11) genes, complete cds
4637	17371		1.01	5.7E-02	M95098.1	NT	EST379865 IMAGE resequences, MAGI Homo sapiens cDNA
7438	20115	33203	0.69	5.7E-02	D78003.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
7438	20115	33204	0.69	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8055	20749	33880	1.42	5.7E-02	AJ290690.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
9750	22401	35608	0.64	5.7E-02	6881280	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
11143	23810	37090	4.42	5.7E-02	AI762695.1	EST_HUMAN	Mus musculus ect2 oncogene (Ect2), mRNA
11143	23810	37091	4.42	5.7E-02	AI762695.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NTFTBC_cn18b09 random
11321	24012		1.59	5.7E-02	AL163303.2	NT	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NTFTBC_cn18b09 random
12265	25213		7.24	5.7E-02	D50320.1	NT	Homo sapiens chromosome 21 segment HS21C103
							Pig DNA for SPAL-2, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12515	25283		3.18	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12650	25387		2.61	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1518	14265	28951	1.57	5.8E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4595	17330	28957	1.12	5.8E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4648	17382	30014	1.46	6.8E-02	AA290599.1	EST_HUMAN	zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6862	19327	32334	6.57	5.8E-02	AW172708.1	EST_HUMAN	x02c10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2856050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN.;
6791	19535	32563	1.25	5.8E-02	AA868182.1	EST_HUMAN	cd47H12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element/contains element L1 repetitive element;
7051	19742	32804	3.05	5.8E-02	BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
7063	19764	32819	0.69	5.8E-02	AI983738.1	EST_HUMAN	W234F05.x1 NCI_CGAP_Bim53 Homo sapiens cDNA clone IMAGE:2559969 3' similar to gb:308408 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
7725	20388	33502	0.69	5.8E-02	AI183583.1	EST_HUMAN	qd84g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1794308 3'
8701	21393	34539	2.89	5.8E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3463279 5'
8701	21393	34540	2.88	5.8E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3463279 5'
9712	22363	35561	1.09	5.8E-02	AA482884.1	EST_HUMAN	mf48d07.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.;
11556	24155		2.35	5.8E-02	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2660	15370	28108	6.9	5.8E-02	X97969.1	NT	H.sapiens gene encoding La autoantigen
3209	15972	28625	3.83	5.8E-02	6755501	NT	Mus musculus SH3 domain protein 1B (SH341B), mRNA
4191	16632	29561	1	5.8E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5573	18370	31281	3.05	5.8E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5635	18370	31281	3.89	5.8E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7277	19961	33038	2	5.8E-02	6755602	NT	Mus musculus tufelin 1 (Tuf1), mRNA
8019	20714	33845	0.63	5.8E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
8019	20714	33846	0.63	5.8E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
9555	22208	35382	0.6	5.8E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9555	22208	35383	0.6	5.8E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9650	22302	35497	1.32	5.8E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
10943	23622	36871	7.26	5.8E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB);>

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12797	25349	30604	1.49	5.6E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3019	15785		0.91	5.4E-02	AJ277488.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3416	17885		5.78	5.4E-02	BE073488.1	EST_HUMAN	RC5-BT0559-140200-012-Q03 BT0559 Homo sapiens cDNA
3891	16841	28281	0.76	5.4E-02	U85808.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8024	20719		0.88	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2385281 to 2613730
8989	21659	34809	0.55	5.4E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10537	23234	36467	1.62	5.4E-02	AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 6'
10598	23292	36530	2.01	5.4E-02	U20780.1	NT	Neurospora crassa ubikulin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11132	23800	37076	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-180700-021-D08 FN0112 Homo sapiens cDNA
11132	23800	37077	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-180700-021-D08 FN0112 Homo sapiens cDNA
1031	13791	26450	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-409 ST0213 Homo sapiens cDNA
1031	13791	26451	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-409 ST0213 Homo sapiens cDNA
1495	14242	26928	14.72	5.3E-02	T94759.1	EST_HUMAN	ye37f12.11 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01508
2501	15218	27961	2.47	5.3E-02	AJ278408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2943	15709	28360	0.95	5.3E-02	M58417.1	NT	Pseudomonas putida tgsS gene
2943	15709	28361	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3150	15913	28558	5.51	5.3E-02	AJ278408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
6029	17749	30361	6.34	5.3E-02	M80463.1	NT	Pseudomonas putida tgsS gene
5236	18042	30670	1.88	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cbx-1) gene, complete cds
5236	18042	30671	1.88	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6785	19529	32556	5.01	5.3E-02	9695413	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6992	19685	32733	1	5.3E-02	U32832.1	NT	Lymphocytis disease virus 1, complete genome
7260	19944		2.06	5.3E-02	S78221.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7777	20399	33514	0.65	5.3E-02	P38742	SWISSPROT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8304	20998		0.7	5.3E-02	U10098.1	NT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
9023	21713	34867	1.56	5.3E-02	X03127.1	NT	Mus musculus 129/Sv cystatin C (cs3) gene, complete cds
10032	22680	35897	0.62	5.3E-02	AB022605.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
10032	22680	35898	0.62	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10166	22804		0.63	5.3E-02	Y07807.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10230	22878	36080	0.7	5.3E-02	X68432.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
							D.rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
							B.rerio pou3c mRNA for transcription factor

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12776	25030	30884	1.43	5.3E-02	AF278815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2283	15008		160.56	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEPTA) mRNA
3112	15877	28516	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3112	15877	28517	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3919	16689	29310	1.23	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
3921	16671		1.19	5.2E-02	6871757	NT	Mus musculus cyclidine inducible SH2-containing protein 3 (Cisf3), mRNA
4245	16986	28609	3.02	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nsr-1 mRNA, complete cds
5053	17772		0.9	5.2E-02	AA297940.1	EST_HUMAN	EST11352 Uterus Homo sapiens cDNA 5' end
5828	18617	31548	0.61	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6016	18797		0.96	5.2E-02	AB830965.1	EST_HUMAN	w80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element
7174	19880	32932	3.13	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8095	20789		2.19	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9629	22282	36472	1.87	5.2E-02	D10927.1	NT	Tumip mosaic virus genomic RNA for Capsid protein, complete cds
9629	22282	35473	1.87	5.2E-02	D10927.1	NT	Tumip mosaic virus genomic RNA for Capsid protein, complete cds
12414	24785		1.93	5.2E-02	D03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2364	15086		1.17	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 5477 (synonym: hifb1) Homo sapiens cDNA clone DKFZp547D073 5'
4178	16919	28547	1.03	5.1E-02	AE007301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4960	17685		49.38	5.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6575	19339	32350	0.72	5.1E-02	AF280369.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds
6780	17929	30584	1.44	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8151	20845	33975	0.84	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8151	20845	33976	0.84	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8245	20939	34076	1.48	5.1E-02	AJ131968.1	NT	Spodoptera littoralis mRNA for 3-dehydrodyscose 3beta-reductase
8783	21475	34622	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8783	21475	34623	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9709	22360	35556	6.2	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10082	22730	35945	1.89	5.1E-02	AF060603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10733	23420	36681	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10733	23420	36682	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11620	24217	37540	1.3	5.1E-02	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/8
12421	24787		2.55	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12678	24988		1.41	6.1E-02	AA534404.1	EST_HUMAN	nt7302.e1 NCI_CGAP_Pt10 Homo sapiens cDNA clone IMAGE:988139
470	13256	25894	1.84	5.0E-02	AF088004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1182	13934	26569	6.54	5.0E-02	Z89104.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
1983	14719	27438	3.81	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FIP-IF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2821	13731	26397	1.28	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3332	16092		1.42	5.0E-02	7305610	NT	Mus musculus Ure-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3582	16337		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3672	16426	29086	5.83	5.0E-02	U12769.2	NT	Arthraea permyl period clock protein homolog mRNA, complete cds
4770	17502		0.99	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6039	18819	31780	0.95	5.0E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6216	18990		1.3	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7437	20114	33202	12.48	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10100	22748	35863	1.28	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
10521	23167		0.45	5.0E-02	BF213280.1	EST_HUMAN	601844763F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070101 5'
11473	24074	37383	2.5	5.0E-02	U67800.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11656	25246		3.5	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
217	13028		24.03	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
360	13158	25800	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
360	13158	25801	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3282	16043	28682	2.53	4.8E-02	P84258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3558	16311		0.69	4.9E-02	AA188940.1	EST_HUMAN	z448a12.s1 Stragene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632828 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3579	16334	28978	0.89	4.9E-02	AA400814.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3579	16334	28979	0.89	4.9E-02	AA400814.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4788	17519	30141	1.91	4.9E-02	AW167821.1	EST_HUMAN	xg58g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386 3'
4788	17519	30142	1.81	4.9E-02	AW167821.1	EST_HUMAN	xg58g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386 3'
5285	18091	30751	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5286	18091	30752	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7042	19733	32783	0.91	4.9E-02	AE000880.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513	21205		0.8	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8652	21344	34489	0.71	4.8E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
10191	22839	36054	0.48	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10494	23140	36366	0.46	4.9E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23885	37285	3.22	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12345	24752		1.77	4.9E-02	8623880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12598	24912		3.41	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
321	13123	25760	1.54	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
322	13123	25760	3.94	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
476	13262	25899	9.96	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2271	14997	27735	1.82	4.8E-02	W51983.1	EST_HUMAN	ze-49b02 s1 Soares, senescent, fibroblasts, NBHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to
3203	15066	28620	2.1	4.8E-02	X17144.1	NT	glo-M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
4623	17358		1.15	4.8E-02	Z54280.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
5144	17863	30478	1.03	4.8E-02	11693131	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5144	17863	30479	1.03	4.8E-02	11693131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
8037	20732	33864	1.32	4.8E-02	AW388497.1	EST_HUMAN	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
9027	21717	34870	0.95	4.8E-02	AJ001398.1	NT	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
9027	21717	34871	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
6731	19585	32597	3.83	4.7E-02	W01153.1	EST_HUMAN	Fugu rubripes rps24 gene
6819	19480	32503	2.02	4.7E-02	M82752.1	NT	y29709.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu
8149	20843	33973	8.24	4.7E-02	X15543.1	NT	repetitive element
8852	21543	34690	0.98	4.7E-02	X99211.1	NT	Rat statin-related protein (s1) gene, complete CDS
8875	21568		2.68	4.7E-02	AB026878.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9127	21815	34981	6.89	4.7E-02	X15543.1	NT	H. sapiens DNA for endogenous retroviral like element
9547	22200	35382	0.67	4.7E-02	BF305237.1	EST_HUMAN	Gallus gallus Wpict-8 gene, complete cds
9635	22287		0.57	4.7E-02	A873042.1	EST_HUMAN	B. taurus mRNA for RF-38-DNA-binding protein
10654	23345	36582	1.4	4.7E-02	U73921.1	NT	601892892F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
11545	24145	37453	1.39	4.7E-02	U73921.1	NT	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11545	24145	37454	1.39	4.7E-02	U73921.1	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
264	13072	25712	0.93	4.6E-02	BE163883.1	EST_HUMAN	Bos taurus paired box protein (pax-6) gene, partial cds
722	13496	26149	2.91	4.6E-02	AE000445.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
1298	14018		0.89	4.6E-02	A014255.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
1338	14088	26762	3.47	4.6E-02	AV727059.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
							am50d02 s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1638979 3' similar to TRP90533
							P90533 LIMA :contains element LTR1 repetitive element;
							AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2492	15209	27951	2.31	4.6E-02	AW238023.1	EST_HUMAN	xn24f03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2884653 3' similar to SW:GRF1_HUMAN
2811	13072	25712	1.9	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1:
3325	15774	28423	0.74	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT03339-251198-003-g05 HT03339 Homo sapiens cDNA
3487	15774	28423	0.73	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT03339-251198-003-g05 HT03339 Homo sapiens cDNA
4103	16846		1.35	4.6E-02	AF220365.1	NT	PMO-HT03339-251198-003-g05 HT03339 Homo sapiens cDNA
5121	17839	30455	0.99	4.6E-02	AA079157.1	EST_HUMAN	Mus musculus nuclear RNA helicase II/Gu (dab21) gene, complete cds
5847	18442	31355	1.57	4.6E-02	AF076982.1	NT	zmf2c10.s1 Striatogene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:545394 3' similar to
6136	18914	31883	3.51	4.6E-02	X81624.1	NT	gb:X03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
6136	18914	31884	3.51	4.6E-02	X81624.1	NT	Haplochromis burtoni gonadotrophin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6702	19617	32659	1.47	4.6E-02	A1149574.1	EST_HUMAN	C.reinhardtii atp2 (atpB) mRNA
8554	21246	34386	2.69	4.6E-02	BE154006.1	EST_HUMAN	C.reinhardtii atp2 (atpB) mRNA
11379	23988	37286	4.94	4.6E-02	AA913328.1	EST_HUMAN	q60b06.x1 Soares placenta, 8to8weeks_2NHP8to9W Homo sapiens cDNA clone IMAGE:1719871 3' similar to contains L1.13 L1 repetitive element;
12325	24744		1.88	4.6E-02	AV712871.1	EST_HUMAN	PMO-HT03339-060400-009-G12 HT03339 Homo sapiens cDNA
12705	24985		3.98	4.6E-02	X57808.1	NT	cd27h09.s1 Soares NFL_T_G8C S1 Homo sapiens cDNA clone IMAGE:1524737 3'
434	13220	25868	1.72	4.5E-02	P22448	SWISSPROT	AV712871 DCA Homo sapiens cDNA clone DCAAZF07 5'
1198	13948	26612	1.11	4.5E-02	AF005730.1	NT	Human germline immunoglobulin lambda light chain gene
1198	13948	26613	1.11	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1797	14537	27247	4.57	4.5E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
2103	14834	27568	3.76	4.5E-02	AE003964.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
3710	18463	28102	3.66	4.5E-02	AL163278.2	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
6137	18915	31885	1.61	4.5E-02	AJ400877.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
6415	19183	32182	0.77	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C078
6779	19523	32550	0.61	4.5E-02	L26487.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6779	19523	32551	0.61	4.5E-02	L26487.1	NT	Homo sapiens chromosome 21 segment HS21C080
8282	20988	34125	1.96	4.5E-02	AF036684.1	NT	Methanoscarcha frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
9849	22499	35689	4.57	4.5E-02	AA325216.1	EST_HUMAN	Methanoscarcha frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
10000	22648	35960	0.48	4.5E-02	X95508.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
							EST/28167 Cerebellum II Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein
							A.europaeum mRNA for legumin-like protein

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10116	22764	35976	0.85	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12154	24640	31097	1.94	4.5E-02	11418013	NT	Homo sapiens rat finger protein-like 3 (RFL3), mRNA
12537	25230	30733	6.81	4.5E-02	AA191097.1	EST_HUMAN	z43f11.11 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632483 5'
213	13025		5.52	4.4E-02	BE972733.1	EST_HUMAN	601662154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2089	14821		5.42	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2494	15211	27653	2.4	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3631	16384	28024	1.95	4.4E-02	AF159160.1	NT	Mycobacterium xenithus serine/threonine kinase Pkt10 (pkt10) gene, complete cds
4584	17319	29945	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4584	17319	29946	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4693	17427		2.28	4.4E-02	AJ226889.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7018	19710	32766	0.64	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7018	19710	32767	0.64	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8680	21342	34486	2.14	4.4E-02	AA736969.1	EST_HUMAN	hw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238221 3'
11007	23679	36936	2.62	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11157	23824	37104	2.78	4.4E-02	AA496739.1	EST_HUMAN	ac33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897031 5'
11890	24460		2.57	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1483 protein, partial cds
12067	25408		1.87	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4107418 5'
763	13536	26195	7.07	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FMSA (FMSA) mRNA, complete cds
2573	15287	28024	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3423	16180	28630	7.84	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3651	16404		1.37	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5152	17689	30482	0.95	4.3E-02	U11788.1	NT	Grapevine fanleaf virus coat protein gene, partial cds
6404	19173	32171	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6404	19173	32172	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6633	19395	32410	0.73	4.3E-02	AA652268.1	EST_HUMAN	ns69c12.s1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188886
8411	21104	34243	0.73	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8700	21392	34537	1.02	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
8700	21392	34538	1.02	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
803	13576	26238	2.7	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
846	13618		2.32	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
878	13845	28315	1.35	4.2E-02	AW003845.1	EST_HUMAN	w34g01.x1 NCI_CGAP_P161 Homo sapiens cDNA clone IMAGE:2645584 3' similar to TR:Q63281 Q63281
1714	14457		1.02	4.2E-02	AL445068.1	NT	L1 RETROPOSON, ORF2 mRNA, contains L1.13 L1 L1 repetitive element;
1771	14513	27213	1.01	4.2E-02	P23081	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3855	16408	28047	2.43	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4100	16843	28471	0.7	4.2E-02	BE282605.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
4284	17023	28648	1.83	4.2E-02	U26674.1	NT	601150933F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
4284	17023	28649	1.83	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (SSG1) gene, complete cds
4885	17428	30060	2.32	4.2E-02	BF342985.1	EST_HUMAN	Saccharomyces cerevisiae general sporulation (SSG1) gene, complete cds
5530	18328	31231	0.68	4.2E-02	AF280107.1	NT	602017105F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4152872 5'
5530	18328	31232	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6888	17892	30517	0.98	4.2E-02	BE288285.1	EST_HUMAN	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7426	20103	33190	4.7	4.2E-02	AF276752.1	NT	601124588F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2886319 5'
8710	21402	34547	9.98	4.2E-02	P05085	SWISSPROT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
10084	22712	35930	1.22	4.2E-02	Q16650	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10989	23845	36898	2.82	4.2E-02	AA976118.1	EST_HUMAN	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
11278	23939	37231	2.54	4.2E-02	BE815822.1	EST_HUMAN	6033511.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290
11278	23939	37232	2.54	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11489	24090	37402	1.68	4.2E-02	AF176458.1	NT	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12415	25335		3.43	4.2E-02	A1863494.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
487	13281	25916	1.24	4.1E-02	AF200628.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
2883	15392	28131	1.04	4.1E-02	AE002330.2	NT	w48g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
4439	17175		7.52	4.1E-02	AW893484.1	EST_HUMAN	Homo sapiens HPS1 gene, intron 5
5558	18353	31262	0.82	4.1E-02	BE251894.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
5558	18353	31263	0.82	4.1E-02	BE251894.1	EST_HUMAN	QV1-NN0012-180400-164-408 NN0012 Homo sapiens cDNA
6783	18527		0.67	4.1E-02	X75881.1	NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343855 5'
6899	19691	32742	1.25	4.1E-02	AE002132.1	NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343855 5'
7413	20090	33174	2.09	4.1E-02		NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
						NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
					7662347	NT	Homo sapiens KIAA0887 protein (KIAA0887), mRNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7502	20173	33285	0.83	4.1E-02	L02110.1	NT	Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7665	20329	33439	3.12	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8541	21233	34376	0.83	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9052	21741	34899	0.81	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
12728	25338	30715	4.07	4.1E-02	AJ271909.1	NT	Brassica napus gin gene for plastid glutamine synthetase, exons 1-12
3238	16000	28850	3.26	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3780	16532	29170	1.27	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5285	18100	30759	5.4	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6120	18898	31866	0.93	4.0E-02	BF110434.1	EST_HUMAN	7n62h07 x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:075296 O75298 R28124.1
7590	20258	33386	6.57	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7650	20314		0.86	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7666	20330	33440	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7668	20330	33441	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8617	21309	34451	2.22	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9544	22197		0.78	4.0E-02	BF679376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9567	22220	35406	4.01	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiofumarate reductase subunit A
9884	22534		1.21	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11778	24368		1.54	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cca+ ATPase
12053	26158	30898	3.31	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1098	19856	26516	2.75	3.9E-02	BF516149.1	EST_HUMAN	U18-BW1-anch-08-0-UJ.s1 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1323	14072	26745	2.45	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1654	14688	27402	2.4	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2708	15415		1.69	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4118	16860	28487	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	16860	29488	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	18207	30813	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystikinin type-A receptor (CCKAR), complete cds
5408	18207	30814	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystikinin type-A receptor (CCKAR), complete cds
5644	18439	31353	1.04	3.9E-02	BE98884.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
5766	18557	31484	0.85	3.9E-02	BF676203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
6957	19439	32454	1.18	3.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7739	20435	33557	1.14	3.9E-02	BF239813.1	EST_HUMAN	601908848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
7959	20654	33778	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
7959	20654	33779	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11388	20398	33511	2	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11913	25298		15.38	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12543	24883		1.83	3.9E-02	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1, TCRBV11S1A1T, HVB relic, TCRBV26S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRB1S1, TCRB1S2, Zinc finger protein 275, Zinc finger protein 82, mtrmq28orf
12668	25223		5.31	3.9E-02	AL049868.2	NT	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
1945	14880	27394	1.16	3.8E-02	BE885137.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
2114	14845		1.77	3.8E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
4876	17603	30228	1.1	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5364	18157	30840	1	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
5996	18777	31739	1.32	3.8E-02	P10284	SWISSPROT	HOMEBOX PROTEIN HOXB4 (HOX-2.6)
7218	19303	32876	1.68	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8582	21254		1.33	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10548	23245	38481	2.62	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
871	13736	26401	4.94	3.7E-02	P16137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1367	14115	28780	0.91	3.7E-02	L14591.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2230	14958	27698	3.84	3.7E-02	AB94806.1	EST_HUMAN	wf85a08.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2494502 3'
2582	15296	28034	0.92	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3045	15911	28457	0.9	3.7E-02	P78944	SWISSPROT	HOMEODERMIN
3047	15913	28458	2.99	3.7E-02	BF312663.1	EST_HUMAN	601886233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3447	16203		1.17	3.7E-02	6880541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
6978	25422		0.83	3.7E-02	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 67

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7592	20260	333088	0.50	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
8914	22503		1	3.7E-02	AA782516.1	EST_HUMAN	af55c08.s1 Soares_parrathyroid_tumor_NbH1PA Homo sapiens cDNA clone 1360912 3'
11854	24506	37811	3.89	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12803	25193	30813	1.94	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3646	16399	29039	1.38	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3654	16407	29046	0.88	3.6E-02	AL086808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5341	18144	30808	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5341	18144	30823	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5413	18212	30821	0.94	3.6E-02	AF181722.1	NT	Homo sapiens RU2AS (RU2) mRNA, complete cds
6807	19370	32382	5.47	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-182-b10 EN0013 Homo sapiens cDNA
6807	19370	32383	5.47	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-182-b10 EN0013 Homo sapiens cDNA
6985	19878	32726	2.5	3.6E-02	AF026952.1	NT	Chromatium vinosum sulfur globule protein Cy2 precursor (sgp2) gene, complete cds
7208	19891	32867	2.78	3.6E-02	AA714521.1	EST_HUMAN	rw20a05.g1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:300314_rna2
7533	20203	33298	1.03	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9291	21958	35130	1.72	3.6E-02	U20608.1	NT	MRO-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
9291	21958	35131	1.72	3.6E-02	U20608.1	NT	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9512	22185	35347	0.83	3.6E-02	BF347588.1	EST_HUMAN	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
11135	23803	37080	1.4	3.6E-02	BF131608.1	EST_HUMAN	602020453F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4166116 5'
11135	23803	37081	1.4	3.6E-02	BF131608.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11862	24436		1.46	3.6E-02	AI280968.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
875	13644	26314	1.08	3.5E-02	U08506.1	NT	q48b09.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1872185 3'
988	13751	26413	1.39	3.5E-02	AF253417.1	NT	Drosophila melanogaster figgin mRNA, complete cds
1558	14303	26891	1.55	3.5E-02	BF678085.1	EST_HUMAN	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1558	14303	26892	1.55	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4188	16929	29559	1.83	3.5E-02	AE001173.1	NT	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4281	17020	29647	1.27	3.5E-02	P53760	SWISSPROT	Thermoplasma maritima section 85 of 136 of the complete genome
6127	18905	31873	1.77	3.5E-02	J01238.1	NT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
							Maize actin 1 gene (Mac1), complete cds

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Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7877	20572		0.78	3.5E-02	H28851.1	EST_HUMAN	yp44a05.r1 Soares retina N25b4HR Homo sapiens cDNA clone IMAGE:180258 5' similar to contains Alu repetitive element;
8521	21213	34357	2.7	3.5E-02	BE958970.1	EST_HUMAN	601844701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3828737 3'
9917	22566	35762	1.45	3.5E-02	X76842.1	NT	Llactis MG1363 grpE and dnaK genes
9985	22813	35817	0.5	3.5E-02	BE561042.1	EST_HUMAN	601344681F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877684 5'
11477	24078	37388	1.82	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291289-002-H03 CT0328 Homo sapiens cDNA
11477	24078	37389	1.82	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291289-002-H03 CT0328 Homo sapiens cDNA
12598	25234		5.69	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
584	13346	25973	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
664	13346	25974	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25973	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25974	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1029	13769	26448	2.92	3.4E-02	AW274020.1	EST_HUMAN	xt26407.x1 Soares NFL_T_G8C S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211 HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1184	13836		7.14	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2391	15112	27849	2.06	3.4E-02	T57160.1	EST_HUMAN	yc20608.r1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3424	16181	28831	1.4	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3757	16509	29145	0.7	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-410 FN0155 Homo sapiens cDNA
3900	16850	28281	3.19	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4559	17264	28822	2.41	3.4E-02	X59798.1	NT	M.musculus S-antigen gene promoter region
5000	17723		3.59	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5019	17740	30349	1.2	3.4E-02	AJ012483.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6764	17823	30558	4.73	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8159	20853		3.25	3.4E-02	AI868628.1	EST_HUMAN	w89404.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
8646	21338	34482	1.36	3.4E-02	AA664888.1	EST_HUMAN	nu70708.e1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
							zq04f11.e1 Stratiogene muscle 837209 Homo sapiens cDNA clone IMAGE:828749 3' similar to TR:G1017425 G1017426
8814	21506		5.97	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRPNTETAEMLTNLKESVTADAGRVEITAANSSGTTKAFINWLDPRG
9678	22330		0.63	3.4E-02	AI082719.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPKYGSGSVTNMYLLKRETSTAVWTEVSATVARTMMKMKL ... ;
363	13161		9.61	3.3E-02	AA398735.1	EST_HUMAN	cd89108.x1 Soares parathyroid tumor_NIH47A Homo sapiens cDNA clone IMAGE:1683519 3'
1143	13898	26559	17.86	3.3E-02	AB035867.1	NT	z75608.e1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728188 3'
							Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1489	14236	26223	1.15	3.3E-02	L16870.1	NT	Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3
1635	14381	27068	1.47	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1732	14474		1.29	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2077	14809		2.48	3.3E-02	R09112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
2453	15171	27910	1.31	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp98 (Traf1), mRNA
4158	14381	27068	2.44	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4435	17171	29800	1.78	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp98 (Traf1), mRNA
6336	19106	32095	27.36	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6336	19106	32096	27.36	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7408	20085	33169	0.63	3.3E-02	AF124182.1	NT	Nicotiana plumbaginifolia molybdopterin synthase sulphuryase (mox5) gene, partial cds
9222	21901	35071	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m82d04.x1 NCJ CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9222	21901	35072	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m82d04.x1 NCJ CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9324	21991	35162	0.68	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9324	21991	35163	0.68	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
11065	23735	37008	3.63	3.3E-02	BF681107.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12142	24630		3.24	3.3E-02	T89545.1	EST_HUMAN	602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
12259	24704		1.52	3.3E-02	AF289695.1	NT	ye49f1.1.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
12288	24718		2.92	3.3E-02	M81890.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
129	12944	25588	0.74	3.2E-02	AJ002005.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
1104	13901	26520	7.01	3.2E-02	AF098275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1104	13901	26521	7.01	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2112	14843		3.01	3.2E-02	P28955	SWISSPROT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
3131	15998	28540	10.08	3.2E-02	BE867353.1	EST_HUMAN	LARGE TEGUMENT PROTEIN
3701	16454	29094	0.92	3.2E-02	AL163203.2	NT	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3942	16592	28330	1.64	3.2E-02	Z74103.1	NT	Homo sapiens chromosome 21 segment HS21C003
3942	16592	28331	1.64	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4193	16934		14.21	3.2E-02	X94768.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4716	17448	30081	3.42	3.2E-02	AF114182.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4894	17621		1.09	3.2E-02	AF108906.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5448	18247	31135	1.83	3.2E-02	X68709.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and amRNP genes, complete cds; G7A gene, partial cds; and unknown genes
							S.griseocarinum whiG-Stv gene

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6448	18247	31136	1.83	3.2E-02	X68709.1	NT	S.griseocaneum whiG-Stv gene
6431	19189	32180	3.13	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
6432	19200		33.46	3.2E-02	T89367.1	EST_HUMAN	yc33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6513	19278	32279	4.14	3.2E-02	AF173845.1	NT	Alu repetitive element; contains LTR1 repetitive element ;
7652	20328	33436	0.84	3.2E-02	11424049	NT	Segutinus oedipus tissue kallikrein gene, complete cds
8169	20893	34030	4.84	3.2E-02	6880566	NT	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8839	21531		0.73	3.2E-02	AF108718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9125	21813	34978	1.21	3.2E-02	AI278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9126	21813	34979	1.21	3.2E-02	AI278971.1	EST_HUMAN	qm17504.X1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9957	22605		4.07	3.2E-02	AA719795.1	EST_HUMAN	qm17504.X1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10256	22804	36114	0.95	3.2E-02	U98762.1	NT	zg54b12.s1 Soares pineal gland N3H-PG Homo sapiens cDNA clone IMAGE:397151 3' similar to
1237	13986		2.14	3.1E-02	4503416	NT	gb1.08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1282	14032	26702	1.72	3.1E-02	P18945	SWISSPROT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1885	14622	27332	1.09	3.1E-02	6871564	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1937	14703		1.34	3.1E-02	Z50087.1	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
5182	17890	30506	1.13	3.1E-02	U78104.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5276	18081		2.12	3.1E-02	AA278478.1	EST_HUMAN	Drosophila melanogaster mRNA for headcase protein
5551	18358	31288	0.74	3.1E-02	BF687742.1	EST_HUMAN	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5828	25072	31338	0.59	3.1E-02	AJ391284.1	NT	zs81a08.L1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
8840	21532	34677	0.46	3.1E-02	BE965092.2	EST_HUMAN	602066783.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 6'
8931	22579	35778	2.93	3.1E-02	AF034778.1	NT	Neisseria meningitidis DNA for region 2 (fhaB- and fhaC-homologs, unknown genes) and flanking genes,
11765	24356	37688	1.78	3.1E-02	6754241	NT	strain FAM18
1619	14368		1.98	3.0E-02	AF187125.1	NT	601658878.R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886281 3'
2500	15304	28040	0.97	3.0E-02	AA402242.1	EST_HUMAN	Enterococcus faecalis surface protein precursor, gene, complete cds
3645	16398	28038	2.78	3.0E-02	AF247644.1	NT	Mus musculus Histidine rich calcium binding protein (Hrc), mRNA
3728	16480		0.74	3.0E-02	AW820223.1	EST_HUMAN	Phycothraes minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3829	16679		1.42	3.0E-02	AA364003.1	EST_HUMAN	z65103.L1 Soares testis NIH Homo sapiens cDNA clone IMAGE:727253 5'
4991	17714	30318	5.83	3.0E-02	AF281074.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
4991	17714	30319	5.83	3.0E-02	AF281074.1	NT	QV2-ST0288-150200-040-e09 ST0288 Homo sapiens cDNA
5307	18112		3.43	3.0E-02	AB046793.1	NT	EST74530 Pineal gland II Homo sapiens cDNA 5' and

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6160	18937	31805	1.4	3.0E-02	N89615.1	EST_HUMAN	z39a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
6160	18937	31806	1.4	3.0E-02	N89615.1	EST_HUMAN	z39a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
6892	19609	32648	3.32	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
6808	19487	32488	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6806	19487	32489	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6871	19453	32472	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6871	19453	32473	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7132	19819	32885	1.4	3.0E-02	MB6524.1	NT	Human dystrophin gene
7483	20155		0.59	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8025	20720		0.48	3.0E-02	BF079708.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295654 5'
8638	21231	34373	0.86	3.0E-02	BF353889.1	EST_HUMAN	IL3-HT0704-280600-108-c04 HT0704 Homo sapiens cDNA
8682	21384		1.8	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	23004	36221	1.49	3.0E-02	AE001787.1	NT	Thermoboga maritima section 108 of 138 of the complete genome
10448	23082	36322	0.49	3.0E-02	Z21211.1	EST_HUMAN	HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11197	23852	37148	2.78	3.0E-02	MB1357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11690	24285	37607	7.75	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCL_CGAP_Kd1 Homo sapiens cDNA clone IMAGE:911263
12243	25389	30618	2	3.0E-02	R32019.1	EST_HUMAN	yf63d04.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:134407 3'
12887	24909		2.46	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
12629	25383		2.06	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Gal-glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2436	15694	27891	1.27	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2890	15756	28402	1.04	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
2890	15756	28403	1.04	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3808	16658	28289	0.89	2.9E-02	H72805.1	EST_HUMAN	y107e10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5972	18754	31715	0.97	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6189	18976	31953	7.39	2.9E-02	BF032233.1	EST_HUMAN	601452861F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3856598 5'
6855	19555	32555	0.56	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flhC-homologs, unknown genes) and flanking genes, strain FAM18
7148	19835	32904	12.03	2.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7897	20592	33723	0.87	2.8E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
7897	20592	33724	0.87	2.8E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
9558	22211	35398	2.49	2.8E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9558	22211	35397	2.49	2.8E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9774	22426		0.76	2.8E-02	AW976897.1	EST_HUMAN	EST388708 MAGe resequencing, MAGN Homo sapiens cDNA
10243	22891	38103	1.25	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 7/7
10877	17902	30590	1.91	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
562	13336		0.96	2.8E-02	AW970163.1	EST_HUMAN	EST382234 MAGe resequencing, MAGK Homo sapiens cDNA
3360	16119	28775	1.3	2.8E-02	AF068083.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3360	16119	28776	1.3	2.8E-02	AF068083.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
5400	18200	30905	11.62	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE3948067 5'
6711	18826	32670	1.16	2.8E-02	T78960.1	EST_HUMAN	y421b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE3948067 5'
8226	20920	34058	1.61	2.8E-02	AJ008820.1	NT	Cratogeomys plantagineum mRNA for homeodomain leucine zipper protein (hbx-1)
8915	21606	34749	0.85	2.8E-02	AA280762.1	EST_HUMAN	zs98c06.r1 NC_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711486 5'
9108	21796	34960	1	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9212	21891	36058	0.69	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12528	25229		1.5	2.8E-02	R05966.1	EST_HUMAN	yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128675 5'
12630	24876		1.48	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S8/13S>
1472	14219	26905	1.23	2.7E-02	U96059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3425	16182	28832	1.74	2.7E-02	AL161494.2	NT	y68h12.r1 Soares_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	16918	28545	1.92	2.7E-02	N47258.1	EST_HUMAN	y68h12.r1 Soares_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	16918	28546	1.92	2.7E-02	N47258.1	EST_HUMAN	y63d09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2864 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
5355	18158	30841	1.2	2.7E-02	R12245.1	EST_HUMAN	T.aestivum pTTH20 mRNA for wheat type V thionin
5812	18601	31529	0.86	2.7E-02	X61670.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
5885	18671	31612	0.64	2.7E-02	AB004789.1	NT	A bisporus pgkA gene
6605	19270		0.93	2.7E-02	X97580.1	NT	
6867	19449	32467	2.29	2.7E-02	AA983571.1	EST_HUMAN	d98f03.g1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1624661 3'

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8252	20946		1.06	2.7E-02	A1377036.1	EST_HUMAN	tc28g08.x1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2085982 3' similar to contains Alu repetitive element;
8514	21206	34349	0.49	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
593	13340	25688	1.12	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2369	16088	27825	3.29	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839585 3'
2368	15090	27827	4.49	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2368	15090	27828	4.49	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2916	15682		1.86	2.6E-02	AF109808.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G8, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4847	17577	30200	2.25	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5005	17728	30332	1.58	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5032	17752	30384	2.35	2.6E-02	AW241154.1	EST_HUMAN	xs52804.x1 NCL_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y089_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069;
6764	18548		0.7	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
5800	18590		0.59	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6125	18903		7.34	2.6E-02	A1206030.1	EST_HUMAN	qg27f11.x1 NCL_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1762317 3'
6331	19101	32089	1.9	2.6E-02	BE621748.1	EST_HUMAN	601483473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6728	19562	32583	0.9	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
6728	19562	32594	0.9	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
6810	19471	32494	7.11	2.6E-02	6881271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
8403	21096	34232	0.71	2.6E-02	AA860946.1	EST_HUMAN	ak22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
8260	22014	35182	1.15	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
8614	22267	35453	0.75	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRR1L Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
8614	22267	35454	0.75	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRR1L Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10303	22850	36165	4.39	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11191	23858		1.67	2.6E-02	4506466	NT	Homo sapiens radixin (RDX) mRNA
11361	24049		2.93	2.6E-02	AA278951.1	EST_HUMAN	zs84c02.r1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:704162 5'
11553	24152	37465	2.2	2.6E-02	AW500547.1	EST_HUMAN	UI-HF-BNO-ekf-e-10-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12170	25375	30615	2.09	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCL_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150944 5'
519	13303	25635	1.75	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
519	13303	25636	1.75	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
791	13563	26224	15.9	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
849	13919	26289	7.2	2.5E-02	BE974314.1	EST_HUMAN	60168036R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950686 3'
2788	15471		2.24	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2856	15722	28371	4.35	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2956	15722	28372	4.35	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4023	17878	29399	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4023	17878	29400	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4182	16922	29650	4.23	2.5E-02	AW692114.1	EST_HUMAN	h36f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5625	18422	31335	0.61	2.5E-02	AT327778.1	EST_HUMAN	z63c10.x5 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:810354 3'
6100	18878		5.01	2.5E-02	BE670128.1	EST_HUMAN	7es0a09.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1 repetitive element
6115	18893		4.1	2.5E-02	BE748888.1	EST_HUMAN	601579333F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6244	19018	31992	1.04	2.5E-02	L28028.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7563	20233	33336	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NC1_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5'
7563	20233	33337	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NC1_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5'
8724	21416	34560	0.81	2.5E-02	Q81713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8863	21554	34688	0.47	2.5E-02	AW025821.1	EST_HUMAN	wa08c10.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516370 3'
8968	22614		0.55	2.5E-02	X71903.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
10482	23128	36356	0.65	2.5E-02	A147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NHIFU Homo sapiens cDNA clone IMAGE:1685982 3'
10712	23401	36840	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
10712	23401	36841	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
10773	23456	36700	2.32	2.5E-02	AJ237836.1	NT	Bos taurus partial stat5B gene, exons 17-19
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Ia alpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-B>
10795	23478		3.48	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
11770	24361		2.55	2.5E-02	AB007548.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA
12134	25311		2.89	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12311	25182		1.76	2.5E-02	11433220	NT	601662365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
12432	24804	31043	1.94	2.5E-02	BE973327.1	EST_HUMAN	y754f11.JT Soares fetal liver spleen 'INFLS Homo sapiens cDNA clone IMAGE:211149 5'
1593	14339	27028	1.7	2.4E-02	H65884.1	EST_HUMAN	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2037	15584	27501	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2037	15584	27502	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4335	17074	29702	1.65	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4485	17220	29847	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4485	17220	29848	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5068	17787	30403	0.95	2.4E-02	8922702	NT	Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA
6121	18999	31867	0.9	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone IMAGE:416791 3'
6267	19040	32016	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6267	19040	32017	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7121	19809	32875	0.8	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX.T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7138	19825	32892	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7138	19825	32893	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7781	20488		0.72	2.4E-02	AW613007.1	EST_HUMAN	RC3-ST0186-230300-019-H06 ST0186 Homo sapiens cDNA
7844	20539		0.5	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8340	21033		0.69	2.4E-02	H78376.1	EST_HUMAN	yv12c05.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element;
8429	21122	34260	9.78	2.4E-02	N69442.1	EST_HUMAN	zb35g11.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294588 3' similar to gb K02909 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element;
8885	21576	34718	0.57	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
							z181c08.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET XTR repetitive element;
8907	21598	34740	0.78	2.4E-02	AA625660.1	EST_HUMAN	AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
9591	22244	35427	0.52	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (crn5) gene, complete cds
9591	22244	35428	0.52	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (crn5) gene, complete cds
9706	22357	35553	2.38	2.4E-02	AV692854.1	EST_HUMAN	AV692854 GKG Homo sapiens cDNA clone GKCDSC03 5'
							rh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element;
9881	22531	35728	2.73	2.4E-02	AA493894.1	EST_HUMAN	60127462F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815802 5'
10512	23158		0.46	2.4E-02	BE387111.1	EST_HUMAN	
11565	24164	37475	1.89	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MufS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11565	24164	37476	1.89	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MufS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11638	24465		2.28	2.4E-02	9627909	NT	Bacteriophage b137, complete genome
12081	24589	31124	1.91	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12136	24625	31094	2.37	2.4E-02	BE928869.1	EST_HUMAN	MRO-F10175-310800-202-806 F10175 Homo sapiens cDNA
12186	24657	31093	1.86	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12188	24857	31104	1.88	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12216	24878		1.34	2.4E-02	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12360	24784		3.88	2.4E-02	AB008589.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1885	14803		4.28	2.3E-02	W05340.1	EST_HUMAN	zab4g08.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:288284 5'
1880	14617		10.45	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2350	15072	27808	2.06	2.3E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
3670	16423	28084	6.18	2.3E-02	Z20377.1	EST_HUMAN	HSAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3702	16455		0.8	2.3E-02	L23429.1	NT	Canis beta-galactosidase-binding lectin (LGALS3) mRNA, 3' end
4129	16871	28488	1.08	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4128	16871	28500	1.06	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4386	17123	28755	0.83	2.3E-02	AW889107.1	EST_HUMAN	GM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4415	17182	28780	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4415	17182	28781	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4416	17880	28782	1.14	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCJ CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4416	17880	28783	1.14	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCJ CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4555	17290	28919	2.56	2.3E-02	BF028487.1	EST_HUMAN	601672278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
4555	17290	28920	2.56	2.3E-02	BF028487.1	EST_HUMAN	601672278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
5291	18098	30758	3.63	2.3E-02	U86303.1	NT	Carlobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6522	19288	32282	4.08	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6883	17859	30613	0.88	2.3E-02	BE141476.1	EST_HUMAN	MRO-HT0080-011099-002-c09 HT0080 Homo sapiens cDNA
7776	20472	33595	6.28	2.3E-02	U69010.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8370	21083	34204	0.94	2.3E-02	AJ288105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8370	21083	34205	0.94	2.3E-02	AJ288106.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8597	21289	34429	0.68	2.3E-02	AJ685380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8597	21289	34430	0.68	2.3E-02	AJ685380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9036	21726	34880	0.98	2.3E-02	P41686	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9759	22410	35617	0.77	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
9829	22571	35776	1.33	2.3E-02	AE000198.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9829	22571	35777	1.33	2.3E-02	AE000198.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10524	23170	36397	0.46	2.3E-02	AF282894.1	NT	Bacillus licheniformis isolate N57N1 KexA gene, partial cds

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10882	23373	38815	2.16	2.3E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12058	25168		5.07	2.3E-02	BE278331.1	EST_HUMAN	601178958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12562	24892	30597	2.18	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12616	25409		2.42	2.3E-02	U11077.1	NT	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12807	25260		1.62	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
720	13494	28147	4.13	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1741	14483		1.38	2.2E-02	4557448	NT	Homo sapiens chromodomain helixase DNA binding protein 2 (CHD2) mRNA
1755	14497	27197	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1755	14497	27198	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
2008	14743	27469	2.13	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
3429	16185		1.49	2.2E-02	AA57795.1	EST_HUMAN	m24a04.s1 NCI_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1084782 3'
3637	16390		4.01	2.2E-02	AA603094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3834	16385	29221	1.28	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3899	16949	29280	0.75	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5006	17729	30333	1.05	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7146	19833	32902	3.63	2.2E-02	AV689721.1	EST_HUMAN	AV689721 GKB Homo sapiens cDNA clone GKBAND03 3'
8269	20863	34104	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8269	20863	34105	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8709	21401	34546	0.82	2.2E-02	X79468.1	NT	P.vulgaris alpha tub 2 mRNA
9586	22239	35422	2.22	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9586	22239	35423	2.22	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10105	22753		0.89	2.2E-02	6878140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11167	23834	37115	1.66	2.2E-02	BE797801.1	EST_HUMAN	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
11841	24425	37768	1.54	2.2E-02	11423632	NT	Homo sapiens transmembrane protein 1 (TMEM1), mRNA
12315	24737		4.07	2.2E-02	AA503553.1	EST_HUMAN	m47n07.s1 NCI_CGAP_Cox3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
410	13195		6.11	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
436	13222		9.98	2.1E-02	AF029726.1	NT	Dictyostellum discoideum histidine kinase C (dhkC) mRNA, complete cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	13889	26858	10.32	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1368	14113	26787	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1368	14113	26788	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1775	14517	27218	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27219	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27220	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2028	14763	27492	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
2028	14763	27493	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
2591	15305	28041	1.32	2.1E-02	AA225095.1	EST_HUMAN	nc21g03.t1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008820
2819	13534	26183	4.48	2.1E-02	N28268.1	EST_HUMAN	y43h107.t1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264541 5'
3147	14763	27492	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3147	14763	27493	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3571	16328	28973	1	2.1E-02	AA461271.1	EST_HUMAN	z63b09.t1 Scores total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:798121 5'
4110	16853	20480	0.81	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4275	17014	29641	0.81	2.1E-02	BF349555.1	EST_HUMAN	802016306F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4151161 5'
4410	17147	29775	1.47	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid gp32-2, erpC and erpD genes, complete cds; and unknown genes
4421	17157	29788	1.53	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4461	17197		0.69	2.1E-02	Y19213.1	NT	Homo sapiens putative psitt-lbA pseudogene for hair keratin, exons 2 to 7
4662	17398	30031	4.51	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4762	17494	30122	1.05	2.1E-02	AL163302.2	NT	Homo sapiens chromosome 21-segment HS21C102
4768	17501	30124	0.76	2.1E-02	AB28432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384628 3'
5553	18350	31259	1.13	2.1E-02	AW378528.1	EST_HUMAN	GM4-HIT0244-111188-040-H05 HIT0244 Homo sapiens cDNA
6866	19448	32466	0.88	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-at12 GN0058 Homo sapiens cDNA
8417	21110	34249	0.8	2.1E-02	9780238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9403	22065	35236	0.5	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628732 3' similar to contains
9531	22184	35368	2.61	2.1E-02	AJ243213.1	NT	Alu repetitive element contains element MER11 repetitive element;
9531	22184	35369	2.61	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9883	22533	35730	1.15	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
						NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
9861	22609	35814	0.69	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628732 3' similar to contains
10522	23168	36395	0.45	2.1E-02	AF001519.1	NT	Alu repetitive element contains element MER11 repetitive element;
						NT	Bacillus halodurans genomic DNA, section 13/14

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11479	24080	37391	1.38	2.1E-02	6754255	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp69a), mRNA
12298	17197		8.62	2.1E-02	Y18213.1	NT	Homo sapiens putative pailHbA pseudogene for hair keratin, exons 2 to 7
12339	25163	30901	1.89	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12714	24988	30989	5.71	2.1E-02	AF163913.1	NT	Azospirillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds
16	12844	25457	1.1	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13
17	12845	25458	14.4	2.0E-02	AW895585.1	EST_HUMAN	MER1 repetitive element ;
252	13081	25689	3.76	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
288	13084	25736	2.72	2.0E-02	AA468838.1	EST_HUMAN	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
781	13553	28214	2.11	2.0E-02	6753635	NT	aa15b10.1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1085	13823	28483	1.6	2.0E-02	AL096805.1	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
1177	13830	28595	1.17	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1177	13830	28596	1.17	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1866	14804	27813	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1866	14804	27814	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2801	15508		3.24	2.0E-02	AL161532.2	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
3077	12844	25457	2.11	2.0E-02	BF002932.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3141	15805		1.4	2.0E-02	7305474	NT	7g51c08.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13
3221	15884		2.35	2.0E-02	AF095588.1	NT	MER1 repetitive element ;
3888	18736	29370	1.3	2.0E-02	M18085.1	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6B), mRNA
5548	18345	31254	0.58	2.0E-02	U34778.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5807	18596	31523	0.7	2.0E-02	L35321.2	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7460	20126	33217	1.11	2.0E-02	AP000004.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
7450	20126	33218	1.11	2.0E-02	AP000004.1	NT	Dictyostelium discoideum class VII unconventional myosin (myoI) gene, complete cds
9777	22428		2.21	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7)
10269	22907	36117	1.62	2.0E-02	A1640342.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7)
10539	23236	36489	1.78	2.0E-02	Z73966.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
11344	24034	37337	2.17	2.0E-02	D88184.1	NT	wat17b02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315 3'
11682	24277	37598	2.21	2.0E-02	10947055	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/182
11682	24277	37599	2.21	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11682	24277	37599	2.21	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11682	24277	37599	2.21	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA

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11880	17009	30595	1.9	2.0E-02	AA456838.1	EST_HUMAN	sa15b10.t1 Soares NIH/MPJ S1 Homo sapiens cDNA clone IMAGE:813307 5'
12336	15508		1.82	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12786	25038		6.4	2.0E-02	T80037.1	EST_HUMAN	y004c09.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5'
677	13452	28095	2.15	1.9E-02	AA572764.1	EST_HUMAN	nt19a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914198 similar to contains L1.t1 L1 repetitive element
1611	14358	27047	1.15	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2032	14767	27496	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2032	14767	27497	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2510	15227	27968	0.97	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2806	15672	28320	7.48	1.9E-02	AA713858.1	EST_HUMAN	mw04405.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1288337 3'
2862	16718	28369	1.66	1.9E-02	AV648668.1	EST_HUMAN	AV648668 GLG Homo sapiens cDNA clone G1CBLH07 3'
3588	18351		1.18	1.9E-02	N52250.1	EST_HUMAN	y228b02.s1 Soares multiple sclerosis 2NblMSP Homo sapiens cDNA clone IMAGE:284331 3'
3681	18444		9.58	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3703	18458	28095	0.85	1.9E-02	AI301183.1	EST_HUMAN	q004c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897280 3' similar to contains Alu repetitive element
4025	18770	28402	1.49	1.9E-02	AF141940.1	NT	Myoplasma imitans VihA1 precursor (VihA1) and VihA2 precursor (VihA2) genes, partial cds
4170	18810	29539	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4170	18810	29540	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4504	17239	28872	3.21	1.9E-02	AI452989.1	EST_HUMAN	i46d04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144651 3' similar to contains Alu repetitive element
4951	15227	27868	4.09	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5233	18039	30867	0.99	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5382	18182	30872	1.41	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5701	18495		0.86	1.9E-02	AB018507.1	NT	Drosophila kenekol gene for glycerol-3-phosphate dehydrogenase, complete cds
7001	19893	32744	1.38	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7001	19893	32745	1.38	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8469	21161		1.23	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome: segment 3/7
9250	21809	35082	1.03	1.9E-02	BF316129.1	EST_HUMAN	601886130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9813	22268	35452	0.6	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9945	22593	35798	1.05	1.9E-02	BF698832.1	EST_HUMAN	601862385F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4076253 5'
10152	22800	36017	0.54	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 2027, 2539000-2544784
10681	23372	36814	1.44	1.9E-02	AF008838.1	NT	Vibrio cholerae V88 phage putative replication protein gene, complete cds
12090	25171	30903	2.82	1.9E-02	AF101085.1	NT	Hirudo medicinalis intermediate filament gilltin mRNA, complete cds
12846	25147		1.36	1.9E-02	L11068.1	NT	Candida albicans lambda C63B fragment

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338	13137	25772	1.4	1.8E-02	AW771104.1	EST_HUMAN	hnr52a08.x1 NCL CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
670	13449	26088	0.83	1.8E-02	BF908122.1	EST_HUMAN	IMER29 repetitive element;
1137	13892	28553	1.32	1.8E-02	X17884.1	NT	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4136983 5'
1416	14164	28847	1.73	1.8E-02	AF243382.1	NT	H.francisci mRNA for myelin basic protein (MBP)
2885	15394	28133	1.71	1.8E-02	AE004544.1	NT	Drosophila melanogaster cytoplasmic protein encode (etc) mRNA, complete cds
3205	16988		0.94	1.8E-02	AE005829.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
4065	16810		0.96	1.8E-02	AA861448.1	EST_HUMAN	hs2a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
4398	17133	29764	1.17	1.8E-02	AW836363.1	EST_HUMAN	ak24404.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408835 3'
6712	18627	32671	5.02	1.8E-02	P14310	SWISSPROT	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
8029	20724	33857	0.88	1.8E-02	U37091.1	NT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
8367	21060	34200	0.91	1.8E-02	AW905327.1	EST_HUMAN	Mus musculus carbonic anhydrase IV gene, complete cds
8410	21103	34242	0.8	1.8E-02	6878943	NT	QV2-NN1073-220400-158-H09 NN1073 Homo sapiens cDNA
9392	22054	35225	0.49	1.8E-02	BF241924.1	EST_HUMAN	Mus musculus microtubule-associated protein 2 (Mtap2), mRNA
9392	22054	35228	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9542	22185		2.41	1.8E-02	AA897543.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9683	22611	35815	1.51	1.8E-02	BE778274.1	EST_HUMAN	af02709.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb1.11872 ZINC FINGER PROTEIN 91 (HUMAN);
10128	22774	35987	1.37	1.8E-02	X96833.1	NT	601463545F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866983 5'
11414	23181	36409	2.31	1.8E-02	AB002337.2	NT	L.stegialis mRNA for myomodulin neuropeptide precursor
11414	23181	36410	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11613	24211	37535	1.59	1.8E-02	AP000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11828	24223	37545	3.32	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (877)
886	13655	25323	1.86	1.7E-02	BE394869.1	EST_HUMAN	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
1783	14524	27230	2.17	1.7E-02	AW573183.1	EST_HUMAN	601310826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1783	14524	27231	2.17	1.7E-02	AW573183.1	EST_HUMAN	hnr34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
1884	14602		3.41	1.7E-02	AL183204.2	NT	L1.1f L1 repetitive element;
2108	14837		10.5	1.7E-02	AB004816.1	NT	Homo sapiens chromosome 21 segment HS21C004
2281	15016	27752	0.99	1.7E-02	S74188.1	NT	Oryctolagus cuniculus mRNA for mitoguinin29, complete cds
2648	15356		1.01	1.7E-02	7657485	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2896	15762	28411	1.44	1.7E-02	AI147616.1	EST_HUMAN	Homo sapiens putative Rab5 GTP/GTP exchange factor homologue (RABEX5), mRNA
							qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696882 3'

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3502	16258		4.67	1.7E-02	AW827388.1	EST_HUMAN	hm45a04.x1 NCL_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3614	16367		0.73	1.7E-02	P04928	SWISSPROT	MER19.b1 MER19 repetitive element; HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4148	16890		1.23	1.7E-02	AA668918.1	EST_HUMAN	ac19f04.s1 Stragene ovary (#837217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu
4176	16916		2.04	1.7E-02	R02506.1	EST_HUMAN	repetitive element; contains element MER24 repetitive element; ye88f08.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:124647 5'
4420	17158	28787	1.49	1.7E-02	AB305278.1	EST_HUMAN	qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881278 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4491	17227	28858	1.78	1.7E-02	AW673188.1	EST_HUMAN	if34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains
4666	17400	30034	1.61	1.7E-02	V00841.1	NT	L1.t1 L1 repetitive element; Messenger RNA for anglerfish (<i>Lophius americanus</i>) scmatostatin II
4763	17495		5.84	1.7E-02	A015076.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840858 3'
5007	17730	30334	0.69	1.7E-02	6881289	NT	Rattus norvegicus N-arginine diase convertase 1 (Nrd1), mRNA
5096	17815		0.91	1.7E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6035	18815	31775	2.07	1.7E-02	AT088247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6484	18251	32250	1.47	1.7E-02	A038280.1	EST_HUMAN	cy85h03.x1 Soares_fetal_liver_spleen_1N1LS_S1 Homo sapiens cDNA clone IMAGE:1872681 3'
6950	19432	32448	1.27	1.7E-02	AF190830.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7103	19791	32856	2.44	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7257	19941	33016	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7257	19941	33017	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7642	20307		1.78	1.7E-02	AJ010770.1	NT	Homo sapiens hyperten gene, exons 1-50
8336	20407	33523	0.98	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
8598	22251	35437	1.3	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434f0314_j1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434f0314 5'
11801	24391	37724	1.38	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE55), mRNA
12631	26337	30716	2.39	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-008 NN1030 Homo sapiens cDNA
498	13282		3.19	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1653	14399	27088	1.04	1.6E-02	Y18880.1	NT	Treponema maltophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue
2246	14974	27711	0.9	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2246	14974	27712	0.9	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2570	15284	28022	1.05	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQT1 gene
2649	16359	28102	1.48	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2669	15408		0.96	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3018	15782	28431	0.71	1.6E-02	AF112282.1	NT	Laccase sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3516	16272	28928	5.9	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3830	16581	28215	1.32	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4154	16998		2.49	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, F-actin-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial
4287	17007	29640	0.97	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-007 PT0012 Homo sapiens cDNA
5538	18334	31241	1.25	1.6E-02	8871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6548	18311	32316	2.05	1.6E-02	AB016281.1	NT	Caendica albicans CaGCR3 gene, complete cds
6832	19494	32517	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
6832	19494	32518	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7610	20276	33384	0.88	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8020	20715	33847	0.76	1.6E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8078	20772		1.88	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapoprotein C-II
9940	22588		2.72	1.6E-02	AF079794.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10319	22968	36184	1.29	1.6E-02	AA572818.1	EST_HUMAN	m19g03.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10319	22968	36185	1.28	1.6E-02	AA572818.1	EST_HUMAN	m19g03.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10826	25132	36748	2.38	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LE0280 (=T16H11))
11174	23841	37124	2.54	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11174	23841	37125	2.54	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11495	24098	37407	1.54	1.6E-02	AJ373558.1	EST_HUMAN	qz28e10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
734	13508		23.05	1.5E-02	8823734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2138	14868	27598	4.24	1.5E-02	N39521.1	EST_HUMAN	yw27b07.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:243925 3'
2172	14901	27635	1.69	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3057	15823	28467	1.6	1.5E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3057	15823	28468	1.6	1.5E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3711	16494	29103	0.98	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
6201	18977	31955	1.56	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
7219	19904		1.63	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7301	19984	33060	1.2	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7773	20469	33592	1.63	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7781	20478	33602	3.59	1.5E-02	11417739	NT	Homo sapiens valyl-RNA synthetase 2 (VARS2), mRNA
8729	21421	34585	0.9	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504 5'
9368	21943		0.61	1.5E-02	AF098774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9470	22078	35251	1.47	1.5E-02	D44808.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9711	22362	35559	0.98	1.5E-02	R32687.1	EST_HUMAN	YH54b10.1 Scores placenta Nb24-IP Homo sapiens cDNA clone IMAGE:133531 5'
9711	22362	35560	0.98	1.5E-02	R32687.1	EST_HUMAN	YH54b10.1 Scores placenta Nb24-IP Homo sapiens cDNA clone IMAGE:133531 5'
11121	23780	37088	3.49	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11183	23830	37109	2.14	1.5E-02	AL111238.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11856	24440	37781	1.38	1.5E-02	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
12277	25214		1.74	1.5E-02	AW760894.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
12787	25039		1.45	1.5E-02	A1763127.1	EST_HUMAN	w08r03.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2398493 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element;
408	13183		2.29	1.4E-02	AE002230.2	NT	Chlamydomonas reinhardtii AR39, section 58 of 84 of the complete genome
1096	13854	26513	4.42	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1234	13983		1.24	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1275	14025		3.77	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1375	14123		1.45	1.4E-02	AF218854.1	NT	Homo sapiens headpin gene, complete cds
1507	14263		1.26	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3207	15970	28822	2	1.4E-02	AF160869.2	NT	Bifidobacterium longum NevH+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminohexose repressor protein (nagCxyR) gene, partial cds
3393	16152	28805	1.07	1.4E-02	AW074212.1	EST_HUMAN	xb08d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'
3478	16234	28888	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3478	16234	28889	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3648	16401	29041	8.63	1.4E-02	6988918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Ef), mRNA
4455	17191	29817	7.77	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGC resequences, MAGG Homo sapiens cDNA
4455	17191	29818	7.77	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGC resequences, MAGG Homo sapiens cDNA
4821	17552	30174	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4821	17552	30175	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6321	18081	32079	5.47	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028860 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6321	19091	32080	5.47	1.4E-02	AA59030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1029880 3' similar to contains Alu repetitive element;
8038	20733		1.94	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37RV complete genome; segment 88/162
8786	21488	34834	0.76	1.4E-02	M81702.1	NT	Candida botulinii methanol oxidase (AOD1) gene, complete cds
8053	21742	34900	0.84	1.4E-02	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9300	21967	35141	2.27	1.4E-02	BE544501.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10455	23101		0.76	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11885	24526	37267	2.2	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12331	24747		1.37	1.4E-02	AF324685.1	NT	Arabidopsis thaliana F21J8.2 mRNA, complete cds
12601	24913		2.36	1.4E-02	11426868	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1948	14683	27385	2.21	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3208	15971	28623	2.23	1.3E-02	BF687081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3208	15971	28624	2.23	1.3E-02	BF687081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3951	16701		1.31	1.3E-02	AF169288.1	NT	Mus musculus beta-saroglycan gene, complete cds
4874	17601	30223	0.83	1.3E-02	U68061.1	NT	Human germine T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBU1S1, TCRBU1S2>
5166	17975	30532	1.31	1.3E-02	AL046868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmoq28orf
5166	17975	30533	1.31	1.3E-02	AL046868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmoq28orf
6072	18851	31816	1.05	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nabp) and survival motor neuron protein (smn) genes, complete cds
6105	18883	31851	0.88	1.3E-02	M62962.1	NT	C.eitnhardtii ribosome 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
6865	17942	30535	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
6865	17942	30536	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7477	20150	33244	4.9	1.3E-02	AJ031593.1	EST_HUMAN	ow05g05.x1 Soares_pseudovirus_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8380	21073	34212	1.65	1.3E-02	AF156861.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10107	22755	35967	1.91	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22826	36040	0.68	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10813	23583	36838	3.97	1.3E-02	AW268563.1	EST_HUMAN	xx04e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'
10913	23583	36839	3.97	1.3E-02	AW268563.1	EST_HUMAN	xx04e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12337	25352		1.44	1.3E-02	289117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599461 to 2812870
12437	24807		2.41	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12607	25145		28.18	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
345	13145	26783	3.48	1.2E-02	AA056286.1	EST_HUMAN	z065g01.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1.1 repetitive element;
440	13226	25869	1.66	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
721	13485	28148	2.02	1.2E-02	AI163522.1	EST_HUMAN	q088r12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element;
2176	14904	27637	1.81	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2178	14907	27640	1.71	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2444	15163	27901	1.39	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2842	16163	27901	1.07	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3098	15863		6.66	1.2E-02	AA075418.1	EST_HUMAN	zn88e03.1 Stratagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:646020 5'
3281	16042	28687	2.1	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3284	16045	28694	0.92	1.2E-02	A668694.1	EST_HUMAN	zb08a07.x1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
4675	17409	30045	0.91	1.2E-02	AI887378.1	EST_HUMAN	wm39f04.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2438335 3'
4859	17588	30211					Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4881	17704		2.03	1.2E-02	U91328.1	NT	Cynops pyrogastris GpUbkqT mRNA, partial cds
6026	17746	30358	1.41	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5888	18461	31375	1.73	1.2E-02	D78588.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6028	18808	31787					Homo sapiens wbcscr1 (WBCSCR1) and wbcscr6 (WBCSCR6) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
6907	19845	32891	0.72	1.2E-02	AF045555.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7192	19878	32952	8.46	1.2E-02	AF175412.1	NT	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7212	19897	32972	1.36	1.2E-02	H02197.1	EST_HUMAN	AV732083 HTF Homo sapiens cDNA clone HTFBUC09 5'
7456	20130	33222	10.54	1.2E-02	AV732093.1	EST_HUMAN	601882848F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065253 5'
			0.57	1.2E-02	BF216850.1	EST_HUMAN	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC8S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA-2) (SIAT4-B)
7696	20591	33722					Homo sapiens fringe protein mRNA, partial cds
8082	20788	33917	2.18	1.2E-02	Q11205	SWISSPROT	
			1.35	1.2E-02	AF193612.1	NT	
8082	20788	33918	1.35	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8788	21480		1.03	1.2E-02	T76887.1	EST_HUMAN	yf72c08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 3'
9539	22192	35376	2.46	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9670	22223	35408	1.35	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12034	24559	31112	2.88	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER)
12615	24922		8.02	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujiiwara) Homo sapiens cDNA clone GEN-557G06 5'
1246	13995	26862	1.49	1.1E-02	AA070364.1	EST_HUMAN	zmf62a1.1.s1 Stratiogene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:530924 3'
1701	14444	27143	1.35	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1701	14444	27144	1.35	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
2031	14768	27495	4.92	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'
2880	15847		4.05	1.1E-02	N99523.1	EST_HUMAN	ze40c06.l1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:285040 5'
3513	18269	28824	2.98	1.1E-02	A1853508.1	EST_HUMAN	tg95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW_XPF_HUMAN
4086	18829		0.86	1.1E-02	AW813786.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4778	17510	30132	1.5	1.1E-02	AL048363.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp568E0924_s1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp568E0924
							Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynab), YnaC (ynac), YnaD (ynad), YnaE (ynae), YnaF (ynaf), YnaG (ynag), YnaH (ynah), YnaI (ynai), YnaJ (ynaj), YnaK (ynak), YnaL (ynal), YnaM (ynam), YnaN (ynan), YnaO (ynao), YnaP (ynap), YnaQ (ynaq), YnaR (ynar), YnaS (ynas), YnaT (ynat), YnaU (ynau), YnaV (ynav), YnaW (ynaw), YnaX (ynax), YnaY (ynay), YnaZ (ynaz), Ynaa (ynaA), Ynab (ynab), Ynac (ynac), Ynad (ynad), Ynae (ynae), Ynaf (ynaf), Ynag (ynag), Ynah (ynah), Ynai (ynai), Ynaj (ynaj), Ynak (ynak), Ynal (ynal), Ynam (ynam), Ynan (ynan), Ynao (ynao), Ynap (ynap), Ynaq (ynaq), Ynar (ynar), Ynas (ynas), Ynat (ynat), Ynau (ynau), Ynav (ynav), Ynaw (ynaw), Ynax (ynax), Ynay (ynay), Ynaz (ynaz), Ynaa (ynaA), Ynab (ynab), Ynac (ynac), Ynad (ynad), Ynae (ynae), Ynaf (ynaf), Ynag (ynag), Ynah (ynah), Ynai (ynai), Ynaj (ynaj), Ynak (ynak), Ynal (ynal), Ynam (ynam), Ynan (ynan), Ynao (ynao), Ynap (ynap), Ynaq (ynaq), Ynar (ynar), Ynas (ynas), Ynat (ynat), Ynau (ynau), Ynav (ynav), Ynaw (ynaw), Ynax (ynax), Ynay (ynay), Ynaz (ynaz)
6057	18837	31789	1	1.1E-02	U68480.1	NT	
7497	20169	33261	2.51	1.1E-02	BE149811.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8538	21230	34372	0.91	1.1E-02	AW988160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8721	21413	34556	0.67	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHIC4040
8800	21492	34639	6.45	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9829	22480	35682	2.03	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.1 Stratiogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
9894	22842	35854	3.55	1.1E-02	AA314895.1	EST_HUMAN	EST186494 Odon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10900	23580	36830	3.23	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBOX5), mRNA
11823	24484		4.16	1.1E-02	AA68239.1	EST_HUMAN	ab77f11.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12678	18829		1.62	1.1E-02	AW813786.1	EST_HUMAN	Alu repetitive element
6	12833	25448	9.16	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1513	14260	26846	1.66	1.0E-02	AW368128.1	EST_HUMAN	MF3-CT0176-111089-003-e10 CT0176 Homo sapiens cDNA
2577	15291		1.67	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041089-017-h12 HT0177 Homo sapiens cDNA
3087	15852	28494	2.7	1.0E-02	BE835556.1	EST_HUMAN	cc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3257	16019	28669	1.49	1.0E-02	BE988999.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3661	16611	29250	0.79	1.0E-02	AJ065086.1	EST_HUMAN	601849967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
							HA0821 Human fetal liver cDNA library Homo sapiens cDNA

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3876	16826	28284	0.7	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4726	17458	30084	4.24	1.0E-02	6753921	NT	Mus musculus corticotrophin releasing hormone receptor 2 (Chr2), mRNA
4763	17524	30146	5.16	1.0E-02	R08567.1	EST_HUMAN	yc54h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198633 5'
5331	18134	30763	0.72	1.0E-02	H52681.1	EST_HUMAN	yc36h11.1 Soares ovary tumor Nbl-HOT Homo sapiens cDNA clone IMAGE:235641 5'
5861	18458	31370	0.57	1.0E-02	AF308388.1	NT	Mus musculus transcription complex subunit NF-A-Tc4 (Nfatc4) gene, exons 1 and 2
6025	18805	31786	1.4	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6086	18866	31831	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6088	18866	31832	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6664	19581	32616	1.92	1.0E-02	Z36842.1	NT	Z mays U3snRNA pseudogene
8293	21980	35133	4.19	1.0E-02	BF036331.1	EST_HUMAN	601458570F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3863177 5'
9293	21980	35134	4.19	1.0E-02	BF036331.1	EST_HUMAN	601458570F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3863177 5'
11228	23892		1.97	1.0E-02	AF167659.1	NT	Citridia fasciculata 27 kDa guinea RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11263	23925		1.48	1.0E-02	AI417981.1	EST_HUMAN	ig55h07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb-X15183_cds1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5 repetitive element;
11340	24030	37394	1.97	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12003	25416		1.83	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12069	25189	30811	3.76	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-H02 DT0007 Homo sapiens cDNA
12075	25243		5.93	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12592	25238		3.74	1.0E-02	X62654.1	NT	H. sapiens gene for Me491/CDX63 antigen
12803	25050	30857	1.84	1.0E-02	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
873	13642	26312	2.1	9.0E-03	AI796128.1	EST_HUMAN	wt4209.x1 NCL CGAP_Kd111 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1241	13980		2.07	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element;
1463	14211	26899	1.1	9.0E-03	AE001270.1	NT	601470242F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3873346 5'
2394	15115	27852	2.48	9.0E-03	AL161556.2	NT	Trepnoma pallidum section 86 of 87 of the complete genome
2403	15124	27861	0.92	9.0E-03	AF089934.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
3659	18412	28050	1.21	9.0E-03	J05184.1	NT	Mus musculus MHC class III protein RPT1 (Rpt1) mRNA, partial cds
4927	17655	30267	1.03	9.0E-03	BE047949.1	EST_HUMAN	S.acidocalcarius thermophilus gene, complete cds
4984	17689	30297	0.95	9.0E-03	T70044.1	EST_HUMAN	tz44e10.y1 NCL CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281468 5'
4984	17689	30298	0.95	9.0E-03	T70044.1	EST_HUMAN	yc17b08.s1 Strabagene lung (#937210) Homo sapiens cDNA clone IMAGE:60919 3'
5720	18512		1.15	9.0E-03	AI809792.1	EST_HUMAN	yc17b08.s1 Strabagene lung (#937210) Homo sapiens cDNA clone IMAGE:60919 3'
6533	19289		4.88	9.0E-03	BE745988.1	EST_HUMAN	wf77f04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7362	20043	33122	0.57	9.0E-03	A1242219.1	EST_HUMAN	qh87c12x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7371	20051	33132	0.8	9.0E-03	8822570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
7774	20470		1.05	9.0E-03	AL036691.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8147	20941		0.65	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9745	22398	35501	0.47	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
9782	22413	35620	1.44	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10907	23587		2.07	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10835	23615	36868	1.57	9.0E-03	BE395980.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
11651	24248	37568	1.55	9.0E-03	L1144.1	NT	Homo sapiens preprogalactin (GAL-1) gene, exons 1, 2, and 3
11651	24248	37569	1.55	9.0E-03	L1144.1	NT	Homo sapiens preprogalactin (GAL-1) gene, exons 1, 2, and 3
12411	25411		2.37	9.0E-03	BE348385.1	EST_HUMAN	hw17609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12703	24983		23.46	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-c09 HT0452 Homo sapiens cDNA
489	13274		4.08	8.0E-03	AA723007.1	EST_HUMAN	zr30603.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains Alu repetitive element
968	13734	26399	36.32	8.0E-03	AF106598.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2154	14984	27617	2.2	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2960	15726		0.93	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mcbA), immunity protein (mtfI), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds
3353	16113	28768	1.08	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3665	16418	29058	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3665	16418	29059	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4350	17089	29721	4.88	8.0E-03	BF363327.1	EST_HUMAN	CMA-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
5083	17802	30420	1.09	8.0E-03	AU140281.1	EST_HUMAN	AU140281 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
5436	18235	30849	2.82	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, lipassin, Raf/GDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
6106	25085	31852	1.45	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
6651	19413	32427	4.89	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE YANA
6820	19481		0.95	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7107	19795	32860	1.79	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7442	20119		2.03	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8781	21473	34619	0.63	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8808	21500	34646	3.29	8.0E-03	AW808682.1	EST_HUMAN	MIR1-ST0111-111189-011-108 ST0111 Homo sapiens cDNA
8816	21508	34653	0.49	8.0E-03	AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 2/8
8878	21569	34713	0.58	8.0E-03	9789968	NT	Mus musculus fusion 2 (human) (Fus2), mRNA
9848	22498		4.63	8.0E-03	BE080509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
10696	23357	36597	1.36	8.0E-03	BE788441.1	EST_HUMAN	501475618F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
10906	23586		3.58	8.0E-03	Z49652.1	NT	S. cerevisiae chromosome X reading frame ORF YJR152w
11715	24309	37632	4.74	8.0E-03	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11814	24402		22.71	8.0E-03	AA010180.1	EST_HUMAN	z632e11.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:380716 5'
11853	24437	37779	1.36	8.0E-03	BF342496.1	EST_HUMAN	602013941F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4148418 5'
11933	24491		1.74	8.0E-03	M89035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
11980	24523		1.74	8.0E-03	AB008161.1	NT	Homo sapiens ABCO31 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
678	13463	26096	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
678	13453	26097	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
966	13721	26397	3.57	7.0E-03	AF243376.1	NT	Glycine max glutiniflone S-transferase GST 21 mRNA, partial cds
1094	13852	26511	3.48	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1343	14091		2.67	7.0E-03	Q61080	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/HH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1374	14122	26797	5.71	7.0E-03	AA668296.1	EST_HUMAN	ab79b08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1491	14238	26924	3.37	7.0E-03	AW303589.1	EST_HUMAN	x121b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1735	14477	27175	1.24	7.0E-03	AW950556.1	EST_HUMAN	EST362626 MAGE resequences, MAGE Homo sapiens cDNA
1735	14477	27176	1.24	7.0E-03	AW950556.1	EST_HUMAN	EST362626 MAGE resequences, MAGE Homo sapiens cDNA
2254	15589	27722	1.86	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3548	16301	28951	0.71	7.0E-03	AI150273.1	EST_HUMAN	q334h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751855 3'
3749	16502	29137	0.8	7.0E-03	AW444463.1	EST_HUMAN	UIH-B13-alk-e-10-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
3782	16544	29179	1.32	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4000	16502	29137	0.83	7.0E-03	AW444463.1	EST_HUMAN	UIH-B13-alk-e-10-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4560	17296		1.24	7.0E-03	AW630888.1	EST_HUMAN	hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869636 5'
4929	17657		2.17	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6729	18521		0.75	7.0E-03	H71106.1	EST_HUMAN	y82g01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6021	25083		4.9	7.0E-03	AW861059.1	EST_HUMAN	gp-X14723 CLUSTERIN PRECURSOR (HUMAN);
6222	18986	31972	1.47	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
							z633f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6443	18211	32207	3.44	7.0E-03	AA327128.1	EST_HUMAN	EST30674 Cdon 1 Homo sapiens cDNA 5' end
6470	18237	32237	0.75	7.0E-03	BE857385.1	EST_HUMAN	7q34b10.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
6878	18504	32529	1.87	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.2 TAR1 repetitive element;
7420	20097	33184	5.48	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7420	20097	33185	5.48	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
8010	20705	33833	2.47	7.0E-03	BE175667.1	EST_HUMAN	S. cerevisiae chromosome II reading frame ORF YBL077w
8511	21203	34348	0.51	7.0E-03	AF281074.1	NT	RC6-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9287	21964		0.75	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
							Homo sapiens serine peptidyl transferase, subunit II gene, complete cds; and unknown genes
9485	22148	35330	0.72	7.0E-03	N52378.1	EST_HUMAN	y40c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246068 3' similar to contains
9620	22273	35460	2.57	7.0E-03	P48982	SWISSPROT	Alu repetitive element
9620	22273	35461	2.57	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10204	22852		1.32	7.0E-03	AV987378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10384	23030		0.77	7.0E-03	A198734.1	EST_HUMAN	AV687379 GKG Homo sapiens cDNA clone GKCAFO07 5'
10729	23417	36658	2.63	7.0E-03	AB008852.1	NT	wc37c09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
10818	23501	36739	1.71	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP62, complete cds
10818	23501	36740	1.71	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
10982	23657		1.29	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12486	24833		1.78	7.0E-03	BE263253.1	EST_HUMAN	Sporobolus stipitatus mRNA for putative glycine and proline-rich protein
12553	24880		1.81	7.0E-03	Y17455.1	NT	601146164F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160478 5'
12681	25400		1.72	7.0E-03	AL163300.2	NT	Homo sapiens LSFR2 gene, penultimate exon
							Homo sapiens chromosome 21 segment HS21C100
1218	13969	26837	12.34	6.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
							SW_PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR;
1218	13969	26838	12.34	6.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
2774	15479	28220	1.3	6.0E-03	AF112374.1	NT	SW_PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR;
2893	15660	28305	3.36	6.0E-03	AA759135.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
2893	15660	28306	3.36	6.0E-03	AA759135.1	EST_HUMAN	sh78a11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
3240	16002		2.22	6.0E-03	H75690.1	EST_HUMAN	sh78a11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
							y77h04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3298	16060		1.31	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3377	16136	28793	1.18	6.0E-03	U60880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, espiapterin reductase and vasodoch

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3377	16138	28794	1.18	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, lectodin, fatty acid binding protein, septaplerin reductase and vasodocin genes, complete cds
3534	16290		1.19	6.0E-03	W37985.1	EST_HUMAN	zot13a11.1 Soares parathyroid tumor NHPA Homo sapiens cDNA clone IMAGE:322172 5'
3552	16405	28044	3.68	6.0E-03	BF510886.1	EST_HUMAN	UHL-B14-epm-c-06-0-UI.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3682	16435	28078	1.08	6.0E-03	BE077350.1	EST_HUMAN	RC1-B10606-280400-014-e07 B10606 Homo sapiens cDNA
3759	16511	28147	1.22	6.0E-03	6754029	NT	Mus musculus glucosaminide-6-phosphate deaminase (Gnp), mRNA
3902	16662	28294	0.76	6.0E-03	AW947284.1	EST_HUMAN	RCO-CT0204-240889-021-b10 CT0204 Homo sapiens cDNA
3938	16888		1.28	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2659513 5'
4331	17070		1.84	6.0E-03	AJ016833.1	EST_HUMAN	ov63ct11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4847	17381	30013	6.67	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Carcibellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5073	17792	30407	2.58	6.0E-03	Q82208	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
6061	25034	31802	0.87	6.0E-03	9627521	NT	Varicella virus, complete genome
6718	19633	32876	1.16	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6755	17824	30559	0.57	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7149	19836	32905	0.61	6.0E-03	AA289442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7149	19836	32906	0.61	6.0E-03	AA289442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7546	20216	33318	0.68	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7702	20365	33479	0.62	6.0E-03	P17984	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
7767	20453	33578	6.9	6.0E-03	AJ033980.1	EST_HUMAN	ov13a04.x1 Soares parathyroid tumor NHPA Homo sapiens cDNA clone IMAGE:1846670 3' similar to contains MER10.b1 MER10 repetitive element;
7874	20569	33685	2.17	6.0E-03	AW798337.1	EST_HUMAN	RCO-UM00651-210300-032-g02 UM0051 Homo sapiens cDNA
7945	20640		1.58	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858628 5'
8454	22004	35178	7.28	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
8943	22591		2.13	6.0E-03	AJ432661.1	EST_HUMAN	t22c02.x1 NCI CGAP_KQ11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW.FR13A_HUMAN
10062	22710	35928	0.86	6.0E-03	AJ011849.1	NT	P40429 80S RIBOSOMAL PROTEIN L13A ;
10184	22842		1.14	6.0E-03	AF084555.1	NT	Bacillus subtilis fndD gene
10304	22951	36166	0.69	6.0E-03	X68366.1	NT	Homo sapiens dectatic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10845	23336	36576	1.75	6.0E-03	AW982184.1	EST_HUMAN	M thermophilicum complete plasmid pFV1 DNA
10713	23402		2.54	6.0E-03	11545814	NT	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
							Homo sapiens hypochthyl zinc finger protein FLJ14011 (FLJ14011), mRNA
10760	23495	36880	1.26	6.0E-03	AJ420786.1	EST_HUMAN	1691c12.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR.O00519 O00519 FATTY ACID AMIDE HYDROLASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10750	23435	36681	1.26	6.0E-03	AI420788.1	EST_HUMAN	tg91c12.x1 NCL CGAP P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE.;
10903	23583		4.6	6.0E-03	U14558.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10904	23584	36833	2.81	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12042	24563		3.25	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12160	25174		6.69	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450298 (section 39 of 148) of the complete genome
12239	25235		3.17	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
12669	24898		1.64	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885388 5'
12588	24910		1.88	6.0E-03	AJ245480.1	NT	Brassica napus alg gene for S-locus glycoprotein, cultivar T2
654	13432	26072	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-RNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	13432	26073	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-RNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26072	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-RNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26073	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-RNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1090	13948	26507	1.15	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2688	15397	28135	2.5	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2636	15702	28351	0.88	5.0E-03	BE266057.1	EST_HUMAN	601194786F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538789 5'
3133	15898	28543	3.82	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3152	15915		2.83	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3184	15927	28575	1.3	5.0E-03	R71794.1	EST_HUMAN	y88g02.s1 Soares breast 2N1bH8t Homo sapiens cDNA clone IMAGE:155666 3'
3272	16033		1.12	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3687	16440	29082	4.03	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3741	16494	29129	0.85	5.0E-03	U39914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3954	16704		1.17	6.0E-03	AA289675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4272	16494	29129	0.82	5.0E-03	U39914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4569	17304	29831	0.73	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4670	17404	30039	1.17	5.0E-03	AJ752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5707	18501	31422	5.5	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6953	18735	31694	2.97	5.0E-03	Q00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y-CHROMOSOME)
6988	18769		0.91	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 62 of 94 of the complete genome
6409	19284		7.58	5.0E-03	BE300091.1	EST_HUMAN	800944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6746	17915	30578	7.45	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6940	19422		0.64	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7385	20885	33143	0.73	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stragene (cat#36206) Homo sapiens cDNA clone HFBOR83 similar to EST containing Alu repeat
7498	20170		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031089-011-07 CT0255 Homo sapiens cDNA
7867	20331	33442	7.5	5.0E-03	AB018816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8119	20813	33948	0.48	5.0E-03	AW856907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8119	20813	33949	0.48	5.0E-03	AW856907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8137	20831	33965	3.29	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECOURSOR (LACTASE)
8509	21201		5.63	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8706	21398	34545	1.04	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
8838	21530	34676	0.71	5.0E-03	M25030.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9482	22135	35315	0.45	5.0E-03	P33760	SWISSPROT	SOF-1 PROTEIN
9739	22380	35595	0.89	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9871	22521	35716	0.7	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10057	22705	35923	0.45	5.0E-03	AA53143.1	EST_HUMAN	h46h10.s1 NCI_CGAP_P49 Homo sapiens cDNA clone IMAGE:995587
10231	22879	36081	0.51	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10377	23023		0.48	5.0E-03	AA653261.1	EST_HUMAN	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
10621	23314		4.99	5.0E-03	T16586.1	EST_HUMAN	684F Heart Homo sapiens cDNA clone 694
10859	23539	36785	3.42	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element;
10859	23539	36786	3.42	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element;
10971	23647	36900	1.89	5.0E-03	T49153.1	EST_HUMAN	y009e04.1 Stragene placenta (4937225) Homo sapiens cDNA clone IMAGE:70686 5'
11021	23693	36956	1.47	5.0E-03	10946753	NT	Mus musculus hypothetical protein, MNCb-4760 (LOC58212), mRNA
11303	23962		3.54	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291622 5'
11774	24365	37697	1.53	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
11774	24365	37698	1.53	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12176	25367		9.26	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12307	24731		4.11	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12409	24792		2.52	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12441	24811		1.67	5.0E-03	AA456597.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12467	25183		2.78	5.0E-03	BF572332.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12643	24940	30980	4.2	5.0E-03	AW449109.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12662	25253		1.76	5.0E-03	Q02388	SWISSPROT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
226	13038	25675	2.98	4.0E-03	AW500196.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
313	13117	25755	2.26	4.0E-03	R46482.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
589	13369	25697	2.69	4.0E-03	AA639339.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
857	13626	26288	2.03	4.0E-03	R46482.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
891	13660		4.64	4.0E-03	AW749101.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
1128	13984	26544	29.46	4.0E-03	AA099777.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
1146	13901	26583	2.4	4.0E-03	AW794740.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
1280	14030	26689	1.57	4.0E-03	AA264374.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
1581	14927		1.52	4.0E-03	AV708305.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
1737	14479	27178	2.23	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2011	14746	27474	10.56	4.0E-03	AA099777.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
2244	14972		2.49	4.0E-03	BE410556.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
2276	15002	27742	1.64	4.0E-03	AW794740.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
2579	15293	28030	1.97	4.0E-03	U52111.2	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
2579	15293	28031	1.97	4.0E-03	U52111.2	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
2698	15405	28140	3	4.0E-03	AJ277365.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
2696	15405	28141	3	4.0E-03	AJ277365.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
2701	15409	28144	1.41	4.0E-03	AL163284.2	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
3219	15982	28634	1.16	4.0E-03	BE154134.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
3219	15982	28635	1.16	4.0E-03	BE154134.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
3521	16277	28931	0.97	4.0E-03	AW188428.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3621	16277	28932	0.97	4.0E-03	AW188426.1	EST_HUMAN	x98804.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:266279 3'
3612	16365	29008	0.73	4.0E-03	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3908	16659	29300	0.73	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tag101) gene, complete cds
3977	16725		1.95	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5057	17776	30393	0.93	4.0E-03	AW103719.1	EST_HUMAN	x883d03.x1 NCI_CGAP_Brm35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.11 L1
5114	17832		0.97	4.0E-03	AA772898.1	EST_HUMAN	L1 repetitive element;
5194	18002	30625	1.8	4.0E-03	AF005859.1	NT	sea73a05.a1 Streptococcus schizo brain S11 Homo sapiens cDNA clone IMAGE:969776 3'
5314	18118	30774	23.91	4.0E-03	AF169825.1	NT	Drosophila melanogaster anan2D7 (anon2D7) mRNA, complete cds
5705	18469	31421	2.48	4.0E-03	P04186	SWISSPROT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5708	18502	31423	1.74	4.0E-03	P21849	SWISSPROT	(HPRG)
5782	18583	31510	0.89	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
5983	18774		4.11	4.0E-03	U22180.1	NT	DKFZp7611014_j1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6140	18918	31898	0.95	4.0E-03	AW590572.1	EST_HUMAN	Rattus norvegicus opsin gene, complete cds
6217	18991	31997	1.6	4.0E-03	BE549453.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2848652 3'
6572	19336	32347	1.28	4.0E-03	AA813222.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461054 5'
6877	19594	32632	1.61	4.0E-03	U78408.1	NT	aj32F11.a1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
6970	19452	32470	0.99	4.0E-03	AL163278.2	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
6970	19452	32471	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7098	19787	32851	3.5	4.0E-03	Q02817	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
7331	20013	33091	1.23	4.0E-03	AI681483.1	EST_HUMAN	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7333	20015	33093	0.78	4.0E-03	BE670170.1	EST_HUMAN	bc37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7424	20101		0.74	4.0E-03	X92109.1	NT	7c31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7943	20538	33686	0.7	4.0E-03	Q9TT92	SWISSPROT	H. sapiens hcgIX gene
7947	20642	33767	5.45	4.0E-03	AF111944.1	NT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS6) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8103	20797	33928	2.06	4.0E-03	7692067	NT	Dicyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8814	21306	34448	6.98	4.0E-03	AI553983.1	EST_HUMAN	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8787	21479		4.25	4.0E-03	AL163209.2	NT	1a49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Aliu
8797	21489	34635	2.97	4.0E-03	AL163278.2	NT	repetitive element;
9827	22478	35679	0.67	4.0E-03	H30684.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
10275	22923	36135	1.3	4.0E-03	AL161555.2	NT	Homo sapiens chromosome 21 segment HS21C078
10466	23112		0.45	4.0E-03	AL163281.2	NT	yp-42g12.J1 Soares retina N255F-R Homo sapiens cDNA clone IMAGE:190150 5'
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
							Homo sapiens chromosome 21 segment HS21C081

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11074	23744	37017	4.09	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
11777	24368	37700	1.82	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12147	25385		1.78	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12167	24649		2.38	4.0E-03	BE288280.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12246	24694		2.27	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BN0-aiip-9-04-0-ULr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12480	24841		3.41	4.0E-03	BF224125.1	EST_HUMAN	7q74c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12521	25283		2.08	4.0E-03	AW614586.1	EST_HUMAN	hh02b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853932 3' similar to contains element LTR5 repetitive element;
12801	25048	30956	2.17	4.0E-03	11436956	NT	Homo sapiens Grb2-associated binder 2 (KJAA0571), mRNA
362	13160	25803	2.38	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
859	13628	26289	5.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1657	14403	27091	3.35	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.e1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2255	14982		1.38	3.0E-03	AF055098.1	NT	Homo sapiens MHC class 1 region
2292	15017		6.44	3.0E-03	Z32621.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
2293	15018	27753	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2293	15018	27754	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3081	15946	28498	3.31	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3149	15912	28557	2.52	3.0E-03	AW802887.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3412	16170	28819	1.72	3.0E-03	U34608.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3420	16177		5.97	3.0E-03	Y12500.1	NT	C. elegans samdc gene
3959	16708	28948	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBG01 5'
3959	16708	28949	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBG01 5'
4016	16762	28990	1.95	3.0E-03	AI792278.1	EST_HUMAN	sh04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4130	16872		1	3.0E-03	Z32521.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
4364	17102	29737	5.63	3.0E-03	AJ011432.1	NT	Rattus norvegicus gahf gene
4428	17164		0.73	3.0E-03	BE3487939.1	EST_HUMAN	h08g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3'
4482	17217	29844	4.97	3.0E-03	AI636141.1	EST_HUMAN	xb8.P10.H3 conom Homo sapiens cDNA 3'
4782	17514	30136	2.38	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Striatogene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4802	17533	30155	7.94	3.0E-03	BE787845.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3895483 5'
5184	17892	30508	3.96	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5468	18267	31159	1.98	3.0E-03	AL249381.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5539	18337	31244	0.99	3.0E-03	U95323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6458	18225	32225	11.75	3.0E-03	AA458701.1	EST_HUMAN	aa13f10.1 Soares NIHIMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7104	19782	32857	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces fragilis pcp13 gene for putative-cytosine permease
7422	20089	33187	3.64	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7839	20534	33681	0.82	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250800-032-007 BT0812 Homo sapiens cDNA
7839	20534	33682	0.82	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250800-032-007 BT0812 Homo sapiens cDNA
8058	20750	33981	1.54	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares parathyroid tumor NBH1PA Homo sapiens cDNA clone IMAGE:304783 3'
8214	20808		0.51	3.0E-03	M63498.1	NT	S. cerevisiae UGA36 gene, complete cds
8360	21053	34194	1.32	3.0E-03	P51889	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8381	21074	34213	1.47	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8485	21177		1.29	3.0E-03	Q9QIM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8890	21581		11.08	3.0E-03	AW613774.1	EST_HUMAN	h180f10.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.1 L1 repetitive element:
8943	21634	34778	4.01	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8967	21657	34808	6.44	3.0E-03	AI016731.1	EST_HUMAN	α03d12.x1 NCL CGAP K103 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_mna1 HISTONE H2B.2 (HUMAN);
8977	21667	34817	0.73	3.0E-03	BF333078.1	EST_HUMAN	602035980F1 NCL CGAP Bim84 Homo sapiens cDNA clone IMAGE:4183938 5'
9309	21978		0.83	3.0E-03	D90901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9347	20418	33538	0.83	3.0E-03	BE154670.1	EST_HUMAN	PM3-HT0344-071299-003-007 HT0344 Homo sapiens cDNA
9536	22189		0.54	3.0E-03	P03355	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9606	22259		3.88	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
9795	22446	35651	1.3	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9898	22546	35740	1.29	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10040	22688	35906	3.97	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10752	23437		1.8	3.0E-03	5803028	NT	Homo sapiens A1P/GTP-binding protein (HEAB), mRNA
11137	20089	33187	2.85	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11353	24043	37346	1.89	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11424	23181	36422	2.52	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11462	24065	37372	2.72	3.0E-03	AF004481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11462	24065	37373	2.72	3.0E-03	AF004481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11543	24143	37452	1.58	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11784	24374		1.48	3.0E-03	AW284812.1	EST_HUMAN	UIH-B12-ah-4-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
11927	25196		2.88	3.0E-03	AI525058.1	EST_HUMAN	promina-5.E07.1 bftumor Homo sapiens cDNA 5'
11982	24510	37256	1.88	3.0E-03	AA983154.1	EST_HUMAN	cr77b10.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER28 repetitive element;
12016	25321		2.28	3.0E-03	AB008898.1	NT	Homo sapiens gene for CNP-N-acetylneuraminic acid hydroxylase, partial cds
12190	24681	31068	2.71	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin38 (cx38 gene)
502	13288	25919	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
502	13286	25920	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	15552		12.31	2.0E-03	T70874.1	EST_HUMAN	Yd15h03.r1 Scores_fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108341 6'
1342	14090	26768	2.07	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1345	14093	26768	1.4	2.0E-03	AA681605.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1354	14102	26777	16.16	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1473	14220	26906	1.73	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1506	14252	26938	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1506	14252	26939	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1586	14332		6.31	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1764	14506	27207	1.13	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1872	14610		1.01	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-06T099-018-003 HT0183 Homo sapiens cDNA
1888	14724	27445	1.57	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2247	14975	27713	1.16	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2558	15272	28007	4.01	2.0E-03	AF167974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2558	15272	28008	4.01	2.0E-03	AF167974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2584	15298		4.57	2.0E-03	AW137782.1	EST_HUMAN	UIH-B11-adi-g-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3411	16169	28818	4.3	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3417	16174	28823	1.13	2.0E-03	BF56865.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3657	16410	29048	6.62	2.0E-03	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4083	16835	29461	1.96	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP36]
4195	16836		11.03	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4393	17130		1.12	2.0E-03	AW297380.1	EST_HUMAN	UIH-BW0-ah-g-03-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4397	17134	29765	0.97	2.0E-03	AI084746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4509	17244	29877	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shorttailed class 2 (shc) mRNA, complete cds
4509	17244	29878	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shorttailed class 2 (shc) mRNA, complete cds
4663	17397		1.84	2.0E-03	R87773.1	EST_HUMAN	yo45a02.s1 Scores adult brain N2b44B55Y Homo sapiens cDNA clone IMAGE:180890 3'
4666	17682	30280	2.57	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5092	17811	30427	1	2.0E-03	BE798380.1	EST_HUMAN	601863004F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937560 5'
5399	18169	30883	1.38	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5540	25070	31245	2.06	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5623	18420	31333	1.86	2.0E-03	U63711.1	NT	Xenopus laevis xefitin mRNA, complete cds
6019	18800	31760	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6019	18800	31761	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6253	19027	32001	2.17	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP)
6253	19027	32002	2.17	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP)
6255	19029	32004	7.5	2.0E-03	BF306187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6291	19084	32046	2.44	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6292	19085	32047	0.98	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6320	19090	32078	1.62	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-RNA synthetase (LysRS)
6508	19271		1.16	2.0E-03	AI991089.1	EST_HUMAN	wu38109.x1 Scores Dleckgraeft ccdn_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;
6541	19308	32311	0.87	2.0E-03	AA677831.1	EST_HUMAN	Z13a11.s1 Scores fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430852 3'
6962	17839	30576	1.52	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
6939	19674	32720	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
6939	19674	32721	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
6981	19506	32531	3.55	2.0E-03	BE067988.1	EST_HUMAN	CMA-BT0368-061298-054-d01 BT0368 Homo sapiens cDNA
7044	19735	32795	0.58	2.0E-03	AI298983.1	EST_HUMAN	qim89d11.x1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7193	19879	32953	0.8	2.0E-03	T86569.1	EST_HUMAN	yd77g10.r1 Scores fetal liver spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114306 5'
7617	20188	33281	1.18	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7650	20645	33769	1.96	2.0E-03	AW592004.1	EST_HUMAN	h97d06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60976 Q60976 JERKY. ;
8116	20810	33944	6.07	2.0E-03	N20287.1	EST_HUMAN	yd42g06.s1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8116	20810	33945	6.07	2.0E-03	N20287.1	EST_HUMAN	y42906.s1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8162	20856	33987	0.54	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C8G9.05 IN CHROMOSOME I
8184	20878	34015	1.19	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239	20833	34069	0.81	2.0E-03	6005855	NT	Homo sapiens Ratina-derived POU-domain factor-1 (RPF-1), mRNA
8239	20833	34070	0.81	2.0E-03	6005855	NT	Homo sapiens Ratina-derived POU-domain factor-1 (RPF-1), mRNA
8264	20958	34097	0.86	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8318	21011		0.91	2.0E-03	AJ40877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8570	21282	34400	0.54	2.0E-03	AB035258.1	NT	Oryctolagus cuniculus mRNA for eukaryotic polypeptide chain release factor 3, partial cds
9094	18419	31331	0.74	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA
9094	18419	31332	0.74	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA
9139	21827	34892	0.84	2.0E-03	AF224889.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9428	22104	35278	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194298 3'
9428	22104	35277	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194298 3'
9458	22008	35178	3.46	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GEMM) (JI) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9566	22219	35404	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9566	22219	35405	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	22276	35484	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9623	22276	35485	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9815	22466	35668	0.81	2.0E-03	AW884268.1	EST_HUMAN	QV3-OT0084-060400-144-e01 OT0084 Homo sapiens cDNA
9942	22590		5.75	2.0E-03	AA251376.1	EST_HUMAN	zs10408.s1 NCI_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
10506	23162	36377	0.45	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141089-012-d01 CT0251 Homo sapiens cDNA
10506	23162	36378	0.45	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141089-012-d01 CT0251 Homo sapiens cDNA
10938	23618		2.97	2.0E-03	M86524.1	NT	Human dystrophin gene
11470	20188	33281	2.58	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11631	24131		2.14	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11638	24138	37446	9.1	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
11809	24473		3.23	2.0E-03	A1625745.1	EST_HUMAN	y65h03.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
11926	24487	37807	2.41	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11949	24502	37810	2.41	2.0E-03	A1084325.1	EST_HUMAN	oy43g06.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TRP97535 P87535 PS-PLA1 PRECURSOR.;
11972	17907		9.37	2.0E-03	A1245167.1	NT	Carnelius dromedarius chrip19 gene for immunoglobulin heavy chain variable region
12172	25361		2.89	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKG Homo sapiens cDNA clone GKGGX005 5'
12282	24707	31050	1.76	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12483	26224		1.48	2.0E-03	A1375037.1	EST_HUMAN	ta6802.x1 Soares fetal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2048061 3' similar to contains Alu repetitive element;
12542	24882		1.64	2.0E-03	AF129768.1	NT	Homo sapiens MSH-55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G8d, G8e, G8f, BAT5, G8b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12713	25175		2.65	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKG Homo sapiens cDNA clone GKGGX005 5'
429	13215	25860	1.28	1.0E-03	H98471.1	EST_HUMAN	y68c08.l1 Soares pituitary_gland_N31-PCG Homo sapiens cDNA clone IMAGE:232334 5'
810	13581	26248	2.31	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TRCQ13825 Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE.;
810	13581	26249	2.31	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TRCQ13825 Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE.;
1073	13831	26489	3.78	1.0E-03	A1866788.1	EST_HUMAN	wk86a08.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1093	13851	26510	1.78	1.0E-03	A1954572.1	EST_HUMAN	wk83e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
2021	14758	27486	3.38	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2150	14880	27614	12.13	1.0E-03	A1131016.1	NT	Homo sapiens SCL gene locus
2879	15745	28393	1.37	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3186	15949	28599	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3186	15949	28600	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3656	16409		1.65	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exon 14, 15
4402	17139	28767	1.28	1.0E-03	BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4441	17177	28803	4.05	1.0E-03	BE246538.1	EST_HUMAN	TCBAP-1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4615	17350	29885	0.84	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4773	17505	30127	1.68	1.0E-03	A1073485.1	EST_HUMAN	ow45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4773	17505	30128	1.68	1.0E-03	A1073485.1	EST_HUMAN	ow45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4774	17506		4.29	1.0E-03	BE164067.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5018	17739	30348	7.24	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5226	18032	30658	1.87	1.0E-03	AA280951.1	EST_HUMAN	z54401.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	18121	30778	3.12	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5369	18170	30856	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG378 isolate) U2-IF2 domain encoding nuclear protein EBNA2, complete cds
5369	18170	30857	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG378 isolate) U2-IF2 domain encoding nuclear protein EBNA2, complete cds
5485	18284	31182	0.83	1.0E-03	BE798491.1	EST_HUMAN	60158841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5491	18280	31187	2.07	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5546	18343	31251	0.67	1.0E-03	N41874.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5546	18343	31252	0.67	1.0E-03	N41874.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5930	18714		2.75	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5968	18750	31711	1.07	1.0E-03	BE963939.2	EST_HUMAN	60165751R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875683 3'
6099	18877		8.78	1.0E-03	11528178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6242	18916	31980	1.14	1.0E-03	T87761.1	EST_HUMAN	y83a11.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:116772 5'
6315	19086		1.7	1.0E-03	AW902585.1	EST_HUMAN	QV3-NIN1024-260400-171-q05 NIN1024 Homo sapiens cDNA
6657	19418	32432	1.37	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7062	19743	32805	2.54	1.0E-03	D16828.1	NT	Human gene for fourth somatostatin receptor subtype
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7639	20209	33308	1.8	1.0E-03	U52111.2	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7698	20274	33382	3.37	1.0E-03	M63378.1	EST_HUMAN	601491081F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3893278 6'
7656	20320	33429	0.98	1.0E-03	BE880044.1	EST_HUMAN	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7789	20494	33608	0.83	1.0E-03	AF274591.1	NT	Homo sapiens partial stearyl-1 gene
7850	20545	33673	5.18	1.0E-03	AL251973.1	NT	z67c09.s1 Soares_pregnat_uterus_Nblm-IPU Homo sapiens cDNA clone IMAGE:460788 3' similar to contains L1.1 L1 repetitive element;
8043	20737	33670	1	1.0E-03	AA122270.1	EST_HUMAN	Homo sapiens exosome-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8142	20836	33668	1.94	1.0E-03	AF163980.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8329	21022	34158	0.68	1.0E-03	U23397.1	NT	z62c06.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34328	0.61	1.0E-03	AA001613.1	EST_HUMAN	z62c06.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34327	0.61	1.0E-03	AA001613.1	EST_HUMAN	z62c06.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8842	21534		1.36	1.0E-03	Y11204.1	NT	V.carleri gene encoding volvoxpsin
8868	21560	34705	0.62	1.0E-03	AW840363.1	EST_HUMAN	CM3-LT0079-170200-092-607 LT0079 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	21688		0.58	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9017	21707	34858	3.88	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cbl subunit mRNA, complete cds
9017	21707	34859	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cbl subunit mRNA, complete cds
9507	22160	35340	1.66	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (egaA) gene, complete cds
9507	22160	35341	1.68	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (egaA) gene, complete cds
9720	22371	35570	0.81	1.0E-03	Q01128	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10083	22711	35929	0.85	1.0E-03	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10088	22716		0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10214	22862	36075	1.72	1.0E-03	AI024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39 b1 MER39 MER39 repetitive element;
10503	23149		0.46	1.0E-03	AA708202.1	EST_HUMAN	eg93f12.s1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element
10503	23259	36495	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181089-011-a09 CT0279 Homo sapiens cDNA
10503	23259	36496	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181089-011-a09 CT0279 Homo sapiens cDNA
10651	23342	36580	2.78	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
10726	23413		3.29	1.0E-03	AI683947.1	EST_HUMAN	tt73a12.x1 NC1_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246448 3' similar to TR:Q28105 Q28105 PVA1 GENE.
10808	23491	36727	1.38	1.0E-03	AW237482.1	EST_HUMAN	xm72d12.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:26889751 3'
11108	23776		3.05	1.0E-03	AV758949.1	EST_HUMAN	AV758949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11905	24470	37805	4.48	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12124	24616		1.38	1.0E-03	AV731520.1	EST_HUMAN	AV731520 HTF Homo sapiens cDNA clone HTFAJG05 5'
12371	25342		1.88	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NC1_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
12478	25365	30612	7.05	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
12821	25187	30809	1.37	1.0E-03	AW947341.1	EST_HUMAN	RCO-CT0205-240689-021-a02 CT0205 Homo sapiens cDNA
5130	17848	30465	0.7	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5596	18391		1.26	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6165	18942		0.6	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6395	19164	32165	0.98	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VARI
9543	22196		1.42	9.0E-04	AB037203.1	NT	Glycerhiza glabra GpdAS1 mRNA for beta-amylin synthase, complete cds
1471	14218		1.02	8.0E-04	X86469.1	NT	X. laevis mRNA for CASR protein

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4159	16899		4.37	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4713	17445	30078	2.39	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11092	23762		2.93	8.0E-04	AA777084.1	EST_HUMAN	Z24c10.s1 Soares fetal heart_NbHH10W Homo sapiens cDNA clone IMAGE:377874 3'
11268	23928		1.98	8.0E-04	A1571089.1	EST_HUMAN	In85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
2398	15119	27866	0.97	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2719	15428	28164	1.19	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3274	16035	28685	1	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6005	18788	31748	0.94	7.0E-04	AA516212.1	EST_HUMAN	reg5g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:839718 similar to contains L1.b3 L1 L1
6420	19188		2.47	7.0E-04	A1709331.1	EST_HUMAN	repetitive element;
7128	19816		0.78	7.0E-04	AK024445.1	NT	wg3609.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
8703	22354	35549	0.53	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00035 protein, partial cds
8703	22354	35550	0.53	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11557	24156		2.28	7.0E-04	U78027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11688	24185	37500	4.04	7.0E-04	Z40561.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12842	24938		2.31	7.0E-04	R17336.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12869	24964		5.98	7.0E-04	6005855	NT	yg13c08.j1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32298 5'
3941	16891	28328	1.83	6.0E-04	AJ862525.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
4068	16812	29440	0.78	6.0E-04	K01315.1	NT	wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4068	16812	29441	0.78	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4162	16902	29531	3.79	6.0E-04	U45983.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
7478	20151	33245	0.61	6.0E-04	Q15034	SWISSPROT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
7785	20461		3.33	6.0E-04	P46408	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7914	20609		0.62	6.0E-04	H92947.1	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
9880	22530		3.5	6.0E-04	AL048507.2	EST_HUMAN	y84c11.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231966 3' similar to contains LOR1 repetitive element;
9880	22528	35837	2.28	6.0E-04	BE005650.1	EST_HUMAN	DKFZp586M2024.J1 586 (synonym: huter) Homo sapiens cDNA clone DKFZp586M2024
10238	22888		0.71	6.0E-04	AF287478.1	NT	RC2-BN0120-250400-012-111 BN0120 Homo sapiens cDNA
11467	24070	37378	2.53	6.0E-04	AJ228042.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds
11658	24157	37467	3.46	6.0E-04	AW013947.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11636	24233		2.17	6.0E-04	Q01768	SWISSPROT	U1H-B10-ead-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
12082	25249		2.81	6.0E-04	AW380519.1	EST_HUMAN	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
							RC1-H10269-261189-012-408 HT0269 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12816	25058		1.34	6.0E-04	AI817088.1	EST_HUMAN	wf76g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408904 3' similar to contains element L1 repetitive element;
636	13415	26051	6.81	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF82)
1490	14237		1.4	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3408	16166	28815	1.35	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3704	16457	28096	2.32	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6386	18186	30877	2.99	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6532	19238	32303	7.89	5.0E-04	AA156080.1	EST_HUMAN	z03308.t1 Stratiogene colon (#837204) Homo sapiens cDNA clone IMAGE:588663 5'
7276	19980	33037	3.75	5.0E-04	M23804.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
							qd13f08.x1 Soares_placenta_869weeks_2N1bHP81b8W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element;
7856	20551	33677	5.2	5.0E-04	AI188382.1	EST_HUMAN	cb98e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339228 3' similar to contains element MER22 repetitive element;
8202	20896	34033	0.96	5.0E-04	AA814519.1	EST_HUMAN	ej59f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9177	21847	35013	1.39	5.0E-04	AA846545.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9271	22025	35195	0.68	5.0E-04	N83765.1	EST_HUMAN	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL A PRECURSOR
9418	22096	35288	1.44	5.0E-04	P28126	SWISSPROT	xs09e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
9509	22162	35344	4.1	5.0E-04	AW270938.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
10177	22825		0.48	5.0E-04	U50871.1	NT	DKFZp586M2024_1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
10897	23577		2.38	5.0E-04	AL048507.2	EST_HUMAN	
11713	18186	30877	14.08	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12020	25184		5.04	5.0E-04	AA568513.1	EST_HUMAN	nf15k02.s1 NCI_CGAP_PT1 Homo sapiens cDNA clone IMAGE:913876
658	13435	26076	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
827	13597	26287	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825 Q13825 AU-BINDING PROTEIN/ENOVYL-COA HYDRATASE.;
827	13597	26288	1.79	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825 Q13825 AU-BINDING PROTEIN/ENOVYL-COA HYDRATASE.;
1449	14198	26880	3.18	4.0E-04	AW753358.1	EST_HUMAN	RCS-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2076	14807	27538	1.81	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2129	14860		1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059.5'
2633	15345	28088	2.21	4.0E-04	O96815	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3162	15925	28572	0.96	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4289	17028	28653	3.18	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
4289	17028	28654	3.18	4.0E-04	AA576331.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4500	17236	28668	1.76	4.0E-04	AA086324.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
5028	17748	30360	3.1	4.0E-04	BE560660.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7168	18655	32926	1.3	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
7434	20111		0.76	4.0E-04	AL161588.2	NT	CALCIUM-SENSING RECEPTOR
7618	20284	33304	0.56	4.0E-04	AU122076.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
8434	21127	34264	1.07	4.0E-04	BF240712.1	EST_HUMAN	AL122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8442	21134	34270	1.5	4.0E-04	N25607.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098700 5'
9590	22243	35426	3.24	4.0E-04	AI025699.1	EST_HUMAN	y639e12.1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:264142 5'
9740	22391		1.22	4.0E-04	AF022855.1	NT	ov87h03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
12380	25157		2.05	4.0E-04	AF234822.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
152	12987	25608	3.48	3.0E-04	AL119428.1	EST_HUMAN	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
180	13003	25644	2.24	3.0E-04	P49259	SWISSPROT	DKFZp761J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
860	13628	26300	1.32	3.0E-04	U83991.1	NT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1831	14570	27282	1.08	3.0E-04	AI282100.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1846	14584		1.21	3.0E-04	AI399674.1	EST_HUMAN	qz28d03.y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
3303	16094	28712	3.43	3.0E-04	P25147	SWISSPROT	h23a02.x1 NCL CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2119082 3'
3308	16098	28717	0.7	3.0E-04	AA203342.1	EST_HUMAN	INTERVALIN B PRECURSOR
3846	16896	28935	4.07	3.0E-04	P49448	SWISSPROT	z656a04.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:446478 5'
4034	16779		1.33	3.0E-04	AJ271735.1	NT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4072	16816		1.12	3.0E-04	BE140609.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
4766	17498		4.72	3.0E-04	BE163778.1	EST_HUMAN	RCO-HT0014-310589-028 HT0014 Homo sapiens cDNA
4827	17558	30180	0.95	3.0E-04	AW837723.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
5063	17782	30399	0.96	3.0E-04	AA613145.1	EST_HUMAN	QV3-DT0045-221289-046-d09 DT0045 Homo sapiens cDNA
8062	18832		7.86	3.0E-04	AL163281.2	NT	ng08g09.s1 NCL CGAP_Lur1 Homo sapiens cDNA clone IMAGE:1143328 3'
8722	19556	32566	2.62	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C081
7491	20163	33256	0.84	3.0E-04	P23468	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
							PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8157	20851	33983	3.23	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9820	22471	35673	1.34	3.0E-04	AA454055.1	EST_HUMAN	2x48kb08.L1 Soares testis NHT Homo sapiens cDNA clone IMAGE:785471 5' similar to gb:M82762
10078	22726	35943	0.85	3.0E-04	A1892139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 18 KD PROTEOLIPID SUBUNIT (HUMAN);
							wf76a11.x1 Soares thymus_NHFT Homo sapiens cDNA clone IMAGE:2513276 3'
10356	23003	36220	3.73	3.0E-04	AA781201.1	EST_HUMAN	a24g05.a1 Soares testis NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S
10465	23141	36387	0.54	3.0E-04	P13816	SWISSPROT	RIBOSOMAL PROTEIN L7A (HUMAN);
11555	24154	37466	1.36	3.0E-04	4501960	NT	GLUTAMIC ACID-RICH PROTEIN PRECURSOR
							Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A), mRNA
11978	26388	30617	4.81	3.0E-04	AA228301.1	EST_HUMAN	nc38a04.L1 NC1 CGAP_Py2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1
12338	26230	30818	3.08	3.0E-04	AB018282.1	NT	repetitive element;
12730	25000		2.75	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
							DKFZp547L185_r1 547 (synonym: fbrt1) Homo sapiens cDNA clone DKFZp547L185 5'
171	12884	26024	2.65	2.0E-04	AF217798.1	NT	Homo sapiens SOG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related
466	13251	26882	1.8	2.0E-04	AU145707.1	EST_HUMAN	protein 1 (ARFRP1) genes, complete cds
887	13656	26324	10.71	2.0E-04	M86524.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
887	13856	26325	10.71	2.0E-04	M86524.1	NT	Human dystrophin gene
							Human dystrophin gene
1156	13911		3.93	2.0E-04	AI288021.1	EST_HUMAN	q18a011.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
1163	13917		2.18	2.0E-04	AL163203.2	NT	MER3.b2 MER3 repetitive element;
1824	14563		1.12	2.0E-04	AF224288.1	NT	Homo sapiens chromosome 21 segment HS21C003
							Mus musculus 5' flanking region of Pite3 gene
							Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relig, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TCRBV1S1, TCRBV1S2>
2561	15295	28033	4.47	2.0E-04	U68061.1	NT	err58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
2868	15762	28398	1.11	2.0E-04	AI124529.1	EST_HUMAN	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3328	16088	28740	1.1	2.0E-04	5174736	NT	QV2-BT0638-070500-194-b07 BT0636 Homo sapiens cDNA
3429	16186	28834	1.98	2.0E-04	BE082317.1	EST_HUMAN	EST360550 MAGE resequences, MAGP Homo sapiens cDNA
3892	16842	28282	0.78	2.0E-04	AW978441.1	EST_HUMAN	Phascolarctus vulgatus nitrate reductase (PNR2) gene, complete cds
4122	16864		4.93	2.0E-04	U01029.1	NT	Phascolarctus vulgatus nitrate reductase (PNR2) gene, complete cds
4620	17355	29690	1.74	2.0E-04	H96265.1	EST_HUMAN	y010111.L1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4620	17355	29691	1.74	2.0E-04	H96265.1	EST_HUMAN	y010111.L1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 6'
4742	17474		1.83	2.0E-04	U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4898	17721	30324	1.1	2.0E-04	AB037987.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6089	17808	30424	1.04	2.0E-04	P5748	SWISSPROT	MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC)
5457	18258	31148	0.73	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDU10 3'
5469	18268	31160	1.75	2.0E-04	AI690882.1	EST_HUMAN	IQ3B11.1 x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2207709 3'
6684	18469	31373	0.98	2.0E-04	AA286852.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
5857	18944	31584	0.81	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6144	18922	31882	0.59	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7130	19818		2.6	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7225	19910		0.55	2.0E-04	AW860963.1	EST_HUMAN	QY0-GT0387-180300-167-910 GT0387 Homo sapiens cDNA
7520	20191		14.88	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7530	20200	33295	1.42	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7855	20550	33675	1.08	2.0E-04	U32444.2	NT	Sclerium lycopersicum phytochrome F (PHYF) gene, partial cds
7855	20550	33678	1.08	2.0E-04	U32444.2	NT	Sclerium lycopersicum phytochrome F (PHYF) gene, partial cds
8182	20878	34012	1.23	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8182	20878	34013	1.23	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8483	21155	34298	1.96	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8842	21334	34478	0.49	2.0E-04	X57331.1	NT	Human immunoglobulin C(nu) and C(delta) heavy chain genes (constant regions)
9293	21912	35083	0.49	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares testis_NHT Homo sapiens cDNA clone 1343518 3'
9319	21988	35158	0.8	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF28.1
9875	22525	35719	1.19	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-161099-011-b05 HT0254 Homo sapiens cDNA
9916	22555	35761	1.77	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742884 5'
10755	23440	36884	5.23	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11128	23786		1.61	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11276	23937	37229	3.06	2.0E-04	A440282.1	EST_HUMAN	ij01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
11403	24052	37356	2.86	2.0E-04	AW196740.1	EST_HUMAN	UH-H-B1-adm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717180 3'
11857	24441	37782	2.77	2.0E-04	AB21304.1	EST_HUMAN	y970b10.x5 Stratiotes ovary (8937217) Homo sapiens cDNA clone IMAGE:77371 3'
1053	13812	28472	3.3	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1092	13850	28508	4.74	1.0E-04	AW013847.1	EST_HUMAN	UH-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1092	13850	28509	4.74	1.0E-04	AW013847.1	EST_HUMAN	UH-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1309	14057		3.12	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1623	14370	27058	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1623	14370	27059	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1854	14592	27308	2.09	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY86
3278	18039	28689	1.08	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68)
3719	16472	29110	0.91	1.0E-04	A1440282.1	EST_HUMAN	g01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
4037	16782	29412	2.11	1.0E-04	IM14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4062	16807	29437	1.15	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLC8BD04 3'
5036	17755	30368	1.28	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5036	17755	30369	1.28	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5769	18560	31487	1.49	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5834	18623	31556	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
5834	18623	31557	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6346	19116	32105	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_Pt3 Homo sapiens cDNA clone IMAGE:252
6738	19572	32605	0.92	1.0E-04	AA584581.1	EST_HUMAN	n25e04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:983486 3' similar to gb:M97252
7088	19776	32841	15.6	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7470	19776	32841	17.82	1.0E-04	AI251980.1	EST_HUMAN	q157d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
7894	20589	33719	0.95	1.0E-04	AA630453.1	EST_HUMAN	q157d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
9236	21915	35038	2.27	1.0E-04	AI806220.1	EST_HUMAN	ab94g08.s1 Stratiene lung (#837210) Homo sapiens cDNA clone IMAGE:854654 3'
9247	21926	35097	1.46	1.0E-04	O88969	SWISSPROT	wf26e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9325	21892		0.49	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9546	22189	35381	1.83	1.0E-04	10863678	NT	y072c08.f1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:113774 5'
10079	22727		2.74	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10115	22763	35975	1	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11312	23971		2.13	1.0E-04	M28587.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11567	24166	37479	2.05	1.0E-04	AW205336.1	EST_HUMAN	Mouse alpha leukocyte interferon gene, complete cds
11667	24166	37480	2.05	1.0E-04	AW205336.1	EST_HUMAN	UH-HB1-ssw-a-02-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
11649	24248	37566	1.76	1.0E-04	AB032868.1	NT	UH-HB1-ssw-a-02-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11692	24287	37609	2.01	1.0E-04	AW269081.1	EST_HUMAN	xv49g12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11725	24319	37643	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11725	24319	37644	2	1.0E-04	Q03698	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12131	25203		2.51	1.0E-04	BE876398.1	EST_HUMAN	712aa10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296058 3' similar to contains L1.13 L1 repetitive element;
882	13457	26102	2.78	9.0E-05	AA18933.1	EST_HUMAN	af45c11.s1 Soares testis NHT Homo sapiens cDNA clone 1282468 3'
1897	14733	27455	1.14	9.0E-05	AW866218.1	EST_HUMAN	QV4-SN0023-070400-168-b04 SN0023 Homo sapiens cDNA
5973	18980	31601	1.81	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7476	20149	33242	0.6	9.0E-05	AW204958.1	EST_HUMAN	UIH-BJ1-ear-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
7476	20149	33243	0.6	9.0E-05	AW204958.1	EST_HUMAN	UIH-BJ1-ear-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9376	21951		3.02	9.0E-05	D86608.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
9378	21853	35125	2.78	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11092	23752	37027	2.69	9.0E-05	AW073078.1	EST_HUMAN	xs34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
11207	23870	37158	1.75	9.0E-05	A287878.1	EST_HUMAN	q123f08.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
11617	18980	31601	3.5	9.0E-05	Q60716	SWISSPROT	MIR repetitive element; PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12178	26259		6.63	9.0E-05	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G5b, G8d, G9a, G9f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, IC7, LST-1, LTB, TNF, and LTA genes, complete cds
802	13574	26237	1.97	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
844	13614		2.75	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2950	15718		0.73	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4448	17184	28808	0.87	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
11099	23769	37045	1.84	8.0E-05	M69197.1	NT	Human hemoglobin and hemoglobin-related protein (HP and HPR) genes, complete cds
12705	25242		4.65	8.0E-05	AA278333.1	EST_HUMAN	zs88f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704553 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
337	13138	25773	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA
337	13138	25774	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA
554	13337	25965	1.1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
554	13337	25966	1.1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1033	13783	26453	1.4	7.0E-05	Q22849	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2724	15431	28168	2.89	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3156	15919	28565	5.72	7.0E-05	AB009080.1	NT	Dictyostelium discoideum gene for TRPA, complete cds
4339	17078	29707	1.71	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4412	17149	29776	0.95	7.0E-05	U60880.1	NT	Caenorhabditis elegans Stp1p homolog mRNA, complete cds
4871	17598	30221	0.71	7.0E-05	9845300	NT	Rat cytomegalovirus Maasricht, complete genome
8124	20818	33854	1.09	7.0E-05	AA505582.1	EST_HUMAN	nt83g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:868086 3'
9453	22003	35175	2.97	7.0E-05	T07085.1	EST_HUMAN	EST04884 Fetal brain, Stratiene (cat#936206) Homo sapiens cDNA clone HFBED60
1112	23782		3.09	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGOE), mRNA
2020	14755	27484	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2020	14755	27485	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2595	15309	28046	1.19	6.0E-05	AI655241.1	EST_HUMAN	nt54h08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2308531 3' similar to gb:J03250 DNA
2690	15399	28137	1.1	6.0E-05	Z84506.1	NT	TOPOISOMERASE I (HUMAN);
2690	15399	28138	1.1	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2817	13440	28080	3.07	6.0E-05	AF053630.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
5822	18611	31541	3.61	6.0E-05	Q12860	SWISSPROT	Homo sapiens monocyte/macrophage elastase inhibitor gene, complete cds
5822	18611	31542	3.61	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6309	18081	32088	1.4	6.0E-05	N72829.1	EST_HUMAN	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6834	19498	32520	0.95	6.0E-05	AA897680.1	EST_HUMAN	y50g11.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:248212 5'
7883	20678	33803	0.76	6.0E-05	BE084410.1	EST_HUMAN	q80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1604588 3'
7883	20678	33804	0.76	6.0E-05	BE084410.1	EST_HUMAN	RCA-BT0311-141189-011-H06 BT0311 Homo sapiens cDNA
8342	21035	34172	0.62	6.0E-05	AA150482.1	EST_HUMAN	RCA-BT0311-141189-011-H06 BT0311 Homo sapiens cDNA
8347	21040	34177	2.22	6.0E-05	AW896628.1	EST_HUMAN	z08c08.s1 Soares_pregnant uterus_Nbr-IPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MIER28 repetitive element;
8478	21171	34319	0.63	6.0E-05	Q60401	SWISSPROT	contains element MIER28 repetitive element;
9151	21882	35050	1.21	6.0E-05	P08607	SWISSPROT	PMA-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
9151	21882	35051	1.21	6.0E-05	P08607	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9421	22089	35271	0.85	6.0E-05	T94149.1	EST_HUMAN	CAB-BINDING PROTEIN PRECURSOR (C4BP)
9621	22274	35462	0.59	6.0E-05	AW627985.1	EST_HUMAN	CAB-BINDING PROTEIN PRECURSOR (C4BP)
10849	23340	36579	3.06	6.0E-05	R75639.1	EST_HUMAN	y28c12.1 Stratiene lung (#837210) Homo sapiens cDNA clone IMAGE:119062 5'
11502	24103	37415	3.36	6.0E-05	AA044015.1	EST_HUMAN	h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
12387	25239	30822	14.34	6.0E-05	AW890110.1	EST_HUMAN	y58a08.s1 Soares placenta Nbr-IPU Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
12810	25053		1.4	6.0E-05	BE858403.1	EST_HUMAN	z158f02.1 Soares_pregnant uterus_Nbr-IPU Homo sapiens cDNA clone IMAGE:487035 5'
1382	14129	26802	10.46	5.0E-05	AW392086.1	EST_HUMAN	MFO-NT00338-250400-001-f08 NT00338 Homo sapiens cDNA
							7g28a08.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3307766 3'
							QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1855	14583		1.2	5.0E-05	8923891	NT	Homo sapiens 220Da peroxisomal membrane protein-like (LOC55885), mRNA
2551	15286	28001	1.1	5.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
3061	16710	29350	2.41	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5074	17793	30408	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5074	17793	30409	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5438	18237	30951	13.38	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6003	18988	31638	3.75	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA06 3'
6078	18955	31822	0.99	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7231	19916		0.87	5.0E-05	AB037884.1	NT	Mus musculus gene for calretinin, exon 1
12175	24810		3.64	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12440	24810		4.72	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2810	13032		3.84	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4449	17185	29809	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4449	17185	29810	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4820	17551		1.16	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
4955	17681	30289	0.75	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
6841	19503	32528	0.74	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9423	22101		7.57	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9801	22550	35745	0.47	4.0E-05	P11369	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10306	22953	36168	0.59	4.0E-05	P23780	SWISSPROT	h338c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element:
10688	23359	36599	4.18	4.0E-05	AW627948.1	EST_HUMAN	xd83e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
12140	24629		1.48	4.0E-05	AW117580.1	EST_HUMAN	z01e11.s1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
12789	25041		1.71	4.0E-05	AA417768.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element:
665	13441	28082	1.6	3.0E-05	AJ248061.1	EST_HUMAN	xx24g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1037	13797	28457	0.86	3.0E-05	AW273851.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1109	13868	26523	1.01	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1109	13968	26524	1.01	3.0E-05	BF037898.1	EST_HUMAN	q91911.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:008632
3287	16048		0.73	3.0E-05	AJ288919.1	EST_HUMAN	008632 GLYCINE TYROSINE-RICH HAIR PROTEIN ;
4349	17088	29719	7.98	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4349	17088	29720	7.98	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4434	17170	29798	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST178986 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4434	17170	29799	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST178986 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4550	17285		0.99	3.0E-05	AL189302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4585	17420	30055	1	3.0E-05	P97488	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4785	13441	26082	0.82	3.0E-05	AI248081.1	EST_HUMAN	chr64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
4791	17522	30144	0.97	3.0E-05	AU125721.1	EST_HUMAN	AU125721 NT2RM4 Homo sapiens cDNA clone NT2RM4002073 5'
5470	18289	31181	1.69	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (MyLc2p), mRNA
6859	19419	32433	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6859	19419	32434	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7789	20494	33616	2.33	3.0E-05	BE733157.1	EST_HUMAN	601597451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8250	20944	34082	1.47	3.0E-05	AA284049.1	EST_HUMAN	z60b05.s1 Stratiogene echizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8791	21483	34630	1.58	3.0E-05	AW770982.1	EST_HUMAN	h194e08.x1 NGL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009838 3'
8796	21487	34633	1.23	3.0E-05	6912431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL-1HY1), mRNA
8799	21491	34638	0.51	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9029	21719		0.56	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9220	21899	35068	1.22	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end
9563	22216		2.92	3.0E-05	AI768331.1	EST_HUMAN	wg36109.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10433	23079	35803	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10433	23079	36304	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12072	24585		1.77	3.0E-05	IL77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2323	15048	27784	1.09	2.0E-05	AI286021.1	EST_HUMAN	q188a11.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2587	15301	28037	2.43	2.0E-05	MI13792.1	NT	MER3.b2 MER3 repetitive element;
2718	15425		7.45	2.0E-05	AA180582.1	EST_HUMAN	Human adenosine deaminase (ADA) gene, complete cds
3134	15593	28544	1.23	2.0E-05	BE068038.1	EST_HUMAN	zq48a12.1 Stratiogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3343	16102	28764	0.93	2.0E-05	AF184614.1	NT	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3362	16121	28776	1.22	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3485	16242		0.71	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
3787	16539		0.78	2.0E-05	AI039107.1	EST_HUMAN	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4643	17377		1.09	2.0E-05	BC378471.1	EST_HUMAN	DKFZp568i064.t1 568 (synonym: h16d2) Homo sapiens cDNA clone DKFZp568i064 5'
5672	18467	31382	1.92	2.0E-05	AJ011712.1	NT	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
							Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5827	18616		0.69	2.0E-05	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
5880	18668	31603	0.78	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
5880	18668	31607	0.78	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6086	18844	31808	0.61	2.0E-05	A1149272.1	EST_HUMAN	qz72a02.x1 Soares placenta_8to9weeks_2Nhl-IP8a9W Homo sapiens cDNA clone IMAGE:1715114 3'
6527	19293	32297	2.28	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
6801	19462	32483	3.27	2.0E-05	Y08928.1	NT	nm06d12.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6814	19475	32497	1.12	2.0E-05	AA492880.1	EST_HUMAN	P.felipianum mRNA for AARP1 protein, partial
6824	19485		9.37	2.0E-05	AI891025.1	EST_HUMAN	Q02711 PRO-POL-DUTPASE POLYPROTEIN;
7053	19744	32808	1.93	2.0E-05	AF224282.1	NT	wu35h07.x1 Soares_Dickgrafe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2622077 3'
7053	19744	32807	1.93	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7267	19851		0.83	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7785	20480	33605	1.71	2.0E-05	A381040.1	EST_HUMAN	Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
9020	21710	34862	0.53	2.0E-05	BE244940.1	EST_HUMAN	tg20h05.x1 NCI CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2108369 3'
9020	21710	34863	0.53	2.0E-05	BE244940.1	EST_HUMAN	TCBAP2E1680 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TCBAP1590
9167	21837	35002	0.58	2.0E-05	P49457	EST_HUMAN	TCBAP2E1680 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TCBAP1590
9167	21837	35003	0.58	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9823	22474	35677	0.49	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10035	22883	35900	0.87	2.0E-05	BF055839.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10457	23103	36333	0.54	2.0E-05	AJ131024.1	NT	7175g09.y1 NCI CGAP_Brm20 Homo sapiens cDNA clone IMAGE:3340578 5'
10457	23103	36334	0.54	2.0E-05	AJ131024.1	NT	Homo sapiens class gene, exon 1-alpha
10489	23135	36332	1.98	2.0E-05	NA1751.1	EST_HUMAN	Homo sapiens class gene, exon 1-alpha
10489	23135	36332	1.98	2.0E-05	NA1751.1	EST_HUMAN	yw61a06.r1 Soares_placenta_8to9weeks_2Nhl-IP8a9W Homo sapiens cDNA clone IMAGE:259570 5'

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10488	23135	36363	1.98	2.0E-05	N41751.1	EST_HUMAN	yw671a06.l1 Soares_placenta_8to9weeks_2nbHP85b9W Homo sapiens cDNA clone IMAGE:269670 5'
10541	19485		2.42	2.0E-05	A1891026.1	EST_HUMAN	yw35f07.x1 Soares_Dieckgraeffe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11287	23948	37243	1.33	2.0E-05	A1493285.1	EST_HUMAN	is30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13638 Q13538 ORF2: FUNCTION UNKNOWN.;
11287	23948	37244	1.33	2.0E-05	A1493285.1	EST_HUMAN	is30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13638 Q13538 ORF2: FUNCTION UNKNOWN.;
11430	23197	36428	2.27	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA ORF2: FUNCTION UNKNOWN.;
12185	25168		4.86	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2.;
12342	25155		2.27	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12674	25247		1.44	2.0E-05	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
2265	14691	27731	3.22	1.0E-05	P27448	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
2700	15603	28143	1.6	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3641	16394	28034	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lembo 120 Suppressor of Hairless (Su(H)) gene, partial cds
3783	16545		1.02	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3949	16699	28037	9.2	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4152	16804	28623	1.2	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4244	16885	28608	2.52	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.l1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4789	17530	30152	1.81	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2866848 3'
6653	19415	32428	1.22	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
6880	19505	32530	2.58	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.H L1 L1 repetitive element.;
6882	19675	32722	3.28	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7677	20341		1.16	1.0E-05	P19474	SWISSPROT	52 KD RO PROTEIN (SJOEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8813	21505		2.24	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8858	21849	34789	3.02	1.0E-05	AA462578.1	EST_HUMAN	z35h112.s1 Soares_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to repetitive element; contains element TAR1 repetitive element.;
9187	21857	35022	12.45	1.0E-05	AA236110.1	EST_HUMAN	gb102382 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9266	22020	35189	0.62	1.0E-05	AV732190.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'
9738	22389	35593	0.74	1.0E-05	AW510902.1	EST_HUMAN	h4k1b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains ORF.t1 ORF repetitive element.;

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9798	22389	35594	0.74	1.0E-05	AW510902.1	EST_HUMAN	h441b02x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFR.H1 OFR repetitive element;
9816	22467	35668	1.16	1.0E-05	AW291521.1	EST_HUMAN	U1H-B12-agk-a-08-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9816	22467	35670	1.16	1.0E-05	AW291521.1	EST_HUMAN	U1H-B12-agk-a-08-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10084	22732		1.87	1.0E-05	AW468995.1	EST_HUMAN	h407c10.x1 NCI CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;
10836	23518	36760	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10836	23518	36761	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11854	24438	37780	1.98	1.0E-05	AF111167.2	NT	Homo sapiens [un dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2678	15387	28129	4.8	9.0E-08	AI683811.1	EST_HUMAN	h73a06.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3092	15857	28498	3.53	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tc9weeks_2N1bHP8b9W Homo sapiens cDNA clone IMAGE:1759181 3'
3597	16350		2.82	9.0E-08	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5815	18604	31532	2.61	9.0E-08	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6765	18509	32534	0.8	9.0E-08	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7340	20021	33069	0.85	9.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7673	20337	33450	13.94	9.0E-08	AI034370.1	EST_HUMAN	ca20g01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1658912 3' similar to contains Alu repetitive element;
8363	21056	34197	1.1	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8881	21572	34715	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8881	21572	34716	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9122	21810	34976	4.3	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10858	23538	36784	3.46	9.0E-06	Q10364	SWISSPROT	POTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2532	15597	27986	1.27	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
10430	23076	36298	0.75	8.0E-06	P34083	SWISSPROT	FASCIQIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10430	23076	36299	0.75	8.0E-06	P34083	SWISSPROT	FASCIQIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
858	13723		2.69	7.0E-06	AA069729.1	EST_HUMAN	ab0010.a1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1419	14167	26851	3.42	7.0E-06	7682177	NT	MER20.11 MER20 repetitive element ; Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2876	15943		5.93	7.0E-06	A368252.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1891298 3' similar to contains Alu repetitive element;
3551	16306		0.92	7.0E-06	AA385542.1	EST_HUMAN	EST198205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5609	18405		5.68	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
5715	18508	31429	1.01	7.0E-06	N98845.1	EST_HUMAN	yy65c07.r1 Soares_multiple_sclerosis_ZN14HMSF Homo sapiens cDNA clone IMAGE:278412 5'
8688	21380	34524	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probe (GS1 gene) (DXF88S1E), mRNA
8800	22451		0.45	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
11930	25358	30608	2.32	7.0E-06	BF218672.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
2918	15684	28329	1.28	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
3680	16433	29076	1.08	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4705	15708	28359	1.91	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4710	17442	30074	2.21	6.0E-06	A1040098.1	EST_HUMAN	aa08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1865738 3' similar to contains MER8.12 MER8 repetitive element ;
5265	18071	30700	1.32	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5324	18127	30787	1.06	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9766	22407		1.48	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
12755	25016	30979	2.27	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1i subunit (CACNA1I), mRNA
5970	18752	31713	3.27	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6245	18019	31993	2.31	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8804 Met protein (M8804 Met), complete cds
7134	19821	32887	1.1	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8359	21052	34192	0.53	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8359	21052	34193	0.53	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10002	22650	35862	6.16	5.0E-06	AA313620.1	EST_HUMAN	EST185498 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10410	23056	36273	0.45	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12649	24953	30887	2.83	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
632	13411	28048	6.1	4.0E-06	R16287.1	EST_HUMAN	ye48c03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
826	13586	28260	7.07	4.0E-06	AW103354.1	EST_HUMAN	xc68g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1311	14059	26733	4.64	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056188 3'
1311	14059	26734	4.64	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056188 3'
1457	14204	26989	1.8	4.0E-06	BF36612.1	EST_HUMAN	QV2-NT0046-200600-250-H07 NT0046 Homo sapiens cDNA
2261	14988	27728	2.17	4.0E-06	AW015401.1	EST_HUMAN	UH-HB10-eat-f-05-O-J1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3060	15828	28471	0.9	4.0E-06	AF198348.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3874	16624	29262	1.05	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4766	17488	30115	1.89	4.0E-06	A1886839.1	EST_HUMAN	w694c10.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432582 3' similar to contains element
8397	21090	34225	0.56	4.0E-06	O16393	SWISSPROT	MER22 repetitive element;
8699	21391	34536	3.56	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
9607	22260	35446	1.24	4.0E-06	AJ272265.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11427	23194	36425	4.21	4.0E-06	AB007855.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2160	14890	27824	1.75	3.0E-06	AA700592.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2160	14890	27825	1.76	3.0E-06	AA700592.1	EST_HUMAN	z344008.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2263	14889		1.44	3.0E-06	AF202635.1	NT	z344008.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2822	15688	28332	1.05	3.0E-06	AA888218.1	EST_HUMAN	Homo sapiens PP1200 mRNA, complete cds
3259	16021		2.05	3.0E-06	A1857778.1	EST_HUMAN	ak48g11.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3763	18515	29152	1.13	3.0E-06	BE047094.1	EST_HUMAN	w22a05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425516 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN contains L1.12 L1 repetitive element;
3763	18515	29153	1.13	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4524	17259	29893	3.74	3.0E-06	X54816.1	NT	hg64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6068	18847	31811	0.93	3.0E-06	AU156412.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
7129	19817		2.43	3.0E-06	P08548	SWISSPROT	AU156412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7981	20676	33801	0.83	3.0E-06	BE562894.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8584	21276	34413	0.68	3.0E-06	P07743	SWISSPROT	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
12349	24755		3.84	3.0E-06	AW385262.1	EST_HUMAN	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
197	13010		2.81	2.0E-06	P54366	SWISSPROT	RCO-LT0001-281199-011-A03 LT0001 Homo sapiens cDNA
1561	14308		4.45	2.0E-06	P21414	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
2376	15098	27638	4.8	2.0E-06	A1672138.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
							w604e03.x1 NCL_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1
							MER30 repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2469	15187	27826	2.37	2.0E-06	P04928	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2571	16285	28023	1.88	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3509	16265	28919	1.12	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLOFDB05 3'
3744	16497	29132	1.59	2.0E-06	AA173518.1	EST_HUMAN	z002a05.t1 Stratiogene ovarian cancer (#37219) Homo sapiens cDNA clone IMAGE:595232 5'
3753	16505	29141	0.82	2.0E-06	AW450215.1	EST_HUMAN	UIH-B19-aky-g-05-Q-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736178 3'
3758	16510	29148	1.82	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5998	18779		0.63	2.0E-06	AA974932.1	EST_HUMAN	cr34h01.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1688609 3' similar to contains Alu repetitive element
6028	18808	31788	0.63	2.0E-06	AI539448.1	EST_HUMAN	ts51f05.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR-Q13537
6348	19118	32108	5.47	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7818	20513		1.63	2.0E-06	AW869223.1	EST_HUMAN	w60b04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7888	20693	33809	0.57	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA
8735	21427		0.6	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
8747	21439	34586	1.8	2.0E-06	H62051.1	EST_HUMAN	z127c11.s1 Scores phreel_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9116	21804	34969	0.82	2.0E-06	AF003629.1	NT	w37c04.t1 Scores ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9116	21804	34970	0.82	2.0E-06	AF003629.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
9136	21823		0.46	2.0E-06	AI473450.1	EST_HUMAN	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
9600	22253	35438	1	2.0E-06	N30576.1	EST_HUMAN	g16g10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
9819	22470		0.63	2.0E-06	AV748969.1	EST_HUMAN	yw68e03.s1 Scores placenta_8tc6weeks_2N6HP8b9W Homo sapiens cDNA clone IMAGE:257212 3'
12251	25357	30609	2.1	2.0E-06	P23249	SWISSPROT	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
32	12860	26477	2.36	1.0E-06	O76082	SWISSPROT	PROTEIN MOV-10
642	13421	28060	2.62	1.0E-06	AF084364.1	NT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1434	14181	28968	1.61	1.0E-06	P09125	SWISSPROT	Mus musculus D6AM5E protein (D6AM5e) mRNA, complete cds
1514	14281	28947	1.67	1.0E-06	AL163278.2	NT	MEROZOITE SURFACE PROTEIN CMZ-8
1584	14311	28987	1.27	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1584	14311	28988	1.27	1.0E-06	AA034141.1	EST_HUMAN	z108a12.s1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element
1578	14325		1.34	1.0E-06	P27625	SWISSPROT	z108a12.s1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element
							DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11733	24328	37650	1.3	9.0E-07	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
4719	17451	30084	3.26	8.0E-07	AL288598.1	EST_HUMAN	q82g07.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
4719	17451	30085	3.26	8.0E-07	AL288598.1	EST_HUMAN	q82g07.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
6798	18887		9.43	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7801	20598		9.73	8.0E-07	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11822	24219		6.59	8.0E-07	U07770.1	EST_HUMAN	EST05660 Fetal brain, Strabagene (cat#336206) Homo sapiens cDNA clone HFBEN89
11812	24478		8.22	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1858	14896	27312	0.91	7.0E-07	AF167341.1	NT	Homo sapiens membrane Interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5432	18231	30844	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30945	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14942	27352	2.88	8.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221089-024-811 CT0277 Homo sapiens cDNA
2496	15213	27858	4.52	8.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKL2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3955	16705		1.83	8.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF-P33 INTERGENIC REGION
9040	21730	34885	1.52	8.0E-07	BF001867.1	EST_HUMAN	7g94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O79820 O79820 4F5L ;
11836	24420	37761	1.3	8.0E-07	BE063509.1	EST_HUMAN	CM0-BT0281-031189-087-803 BT0281 Homo sapiens cDNA
12166	26307		2.28	8.0E-07	AW903222.1	EST_HUMAN	CM4-NN1028-260300-121-112 NN1028 Homo sapiens cDNA
318	13121		1.94	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1035	13765		4.25	5.0E-07	AA380630.1	EST_HUMAN	EST93815 Supt cells Homo sapiens cDNA 5' end
3028	15784		0.88	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6028	18809	31769	0.9	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6864	19446	32463	1.69	5.0E-07	AI939391.1	EST_HUMAN	ig06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
6864	19446	32464	1.69	5.0E-07	AI939391.1	EST_HUMAN	ig06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
7248	19833	33008	17	5.0E-07	AW070885.1	EST_HUMAN	xa31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:26588362 3' similar to gb:U16341
8173	20867	33969	0.74	5.0E-07	O6WUQ1	SWISSPROT	CYTCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8388	21081		0.82	5.0E-07	P09593	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
10265	22913	36123	4.94	5.0E-07	AI908587.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
							CM-BT178-220498-014 BT178 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10560	23256	38493	1.28	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11500	24101	37413	4.04	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11574	24173		2.62	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12561	25211		3.48	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
3381	16728	28384	2.02	4.0E-07	AW008932.1	EST_HUMAN	ws84h05.x1 NCI_C3GAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
7078	19769		0.83	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7167	19854	32923	1.74	4.0E-07	Q822V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE M-HDA1)
7167	19854	32924	1.74	4.0E-07	Q822V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE M-HDA1)
7823	20518	33644	0.6	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8949	21840	34787	5.41	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10027	22875	35890	0.47	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956651 5'
10027	22875	35891	0.47	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956651 5'
10223	22871	36084	0.49	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10856	23536	36781	3.14	4.0E-07	AJ785528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
10856	23536	36782	3.14	4.0E-07	AJ785528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11184	23849		1.68	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
431	13217	25882	9.64	3.0E-07	U19719.1	NT	Human microtubulin-associated glycoprotein (MFA2) gene, putative promoter region and alternatively spliced untranslated exons
569	13350	25978	2.12	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1353	14101	26776	2.67	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
1622	14369		2.03	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2039	14773		1.42	3.0E-07	AA526763.1	EST_HUMAN	ni56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:380825 similar to contains AU repetitive element contains L1.13 L1 repetitive element
2286	15011	27749	1.83	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2472	15180	27830	7.61	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2472	15180	27831	7.61	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3031	15797	28443	1.16	3.0E-07	T84704.1	EST_HUMAN	yd50f12.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111695 6'
3157	15920	28568	1.45	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RM1 INTERGENIC REGION PRECURSOR
4678	17412	30047	7.42	3.0E-07	AV650201.1	EST_HUMAN	AV650201 G1C Homo sapiens cDNA clone GLCGCD01 3'
4711	17443	30075	0.86	3.0E-07	AJ787236.1	EST_HUMAN	ws86b12.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2347987 3'
5004	17727	30330	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.e1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5004	17727	30331	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5580	18377	31280	12.43	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
5883	18669	31610	0.83	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6603	19368		6.57	3.0E-07	AA815175.1	EST_HUMAN	cc04c10.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7409	20088	33170	3.48	3.0E-07	AW787188.1	EST_HUMAN	QV1-UM0038-200300-115-g02 UM0036 Homo sapiens cDNA
7581	20231		0.79	3.0E-07	AF591065.1	EST_HUMAN	hw28f11.x1 NC1_CGAP_Ov36 Homo sapiens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
8028	21718	34872	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9028	21718	34873	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11484	24085		1.45	3.0E-07	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
11658	24253		1.75	3.0E-07	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
12781	25043		5.1	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
27	12855	25471	4.15	2.0E-07	AF262888.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
150	12865	25608	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
150	12865	25607	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
177	12889	25629	44.15	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
731	13505	26180	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	13505	26161	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
744	13517		0.82	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
922	13689	26353	3.73	2.0E-07	AA223280.1	EST_HUMAN	zr08b07.s1 Stratiene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650868 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
923	13690	26354	2.15	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratiene lung (#837210) Homo sapiens cDNA clone IMAGE:50780 3' similar to contains L1 repetitive element;
1140	13695	26556	1.37	2.0E-07	Q26768	SWISSPROT	U6 AUTOANTIGEN
1598	14342	27032	2.08	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3676	19429	29070	15.93	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5059	17778	30395	0.84	2.0E-07	AW070965.1	EST_HUMAN	xa05h07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2667485 3' similar to WP:C3842.1 CE00923 PROBABLE RABGAP DOMAINS ;

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5059	17778	30396	0.84	2.0E-07	AW070985.1	EST_HUMAN	z65h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38421
5280	18068	30694	1.21	2.0E-07	AW880686.1	EST_HUMAN	CE000923 PROBABLE RABGAP DOMAINS ;
6456	25090	32223	0.81	2.0E-07	AW448688.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6565	16330	32337	1.79	2.0E-07	AI208715.1	EST_HUMAN	UHL-B13-aka-b-01-Q-UJ.1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2794008 3'
7568	20238	33342	0.67	2.0E-07	X95159.1	NT	gg56405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8369	21062		4.08	2.0E-07	AV728390.1	EST_HUMAN	HLsapiens brca2 gene exon 9
8695	21287	34426	0.97	2.0E-07	AA035198.1	EST_HUMAN	AV728390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9661	22313		2.8	2.0E-07	AL163303.2	NT	z627g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10167	22815	36033	5.41	2.0E-07	AW892507.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G103
10388	23032	36245	0.9	2.0E-07	P00751	SWISSPROT	CMA-NN0003-280300-124-408 NN0003 Homo sapiens cDNA
10988	23032	36246	0.9	2.0E-07	P00761	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
11871	24945		2.44	2.0E-07	BE163717.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11953	25212		2.39	2.0E-07	AI732462.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
1080	13838		1.97	1.0E-07	AL163282.2	NT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
2381	15103	27842	1.11	1.0E-07	P10263	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
2830	14259	28945	2.51	1.0E-07	P00258	SWISSPROT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
3727	13838		1.29	1.0E-07	AL163282.2	NT	PM0-HT0339-280100-006-H07 HT0339 Homo sapiens cDNA
4260	17001	29631	2.76	1.0E-07	AV718662.1	EST_HUMAN	z785h11.x5 Strabegene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565028 3' similar to
4260	17001	29632	2.76	1.0E-07	AV718662.1	EST_HUMAN	contains THR.b2 THR repetitive element ;
4680	17424		0.93	1.0E-07	O75820	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
5072	17791	30406	0.93	1.0E-07	AA019181.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							GLYCOPROTEIN GPV
							Homo sapiens chromosome 21 segment HS21C082
							AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
							AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
							ZINC FINGER PROTEIN 189
							z65g02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363026 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Lb
6410	19178	32177	0.87	1.0E-07	U82671.2	NT	z63406.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2281339 5'
6768	19512	32537	5.24	1.0E-07	BE047871.1	EST_HUMAN	z63406.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2281339 5'
6768	19512	32538	5.24	1.0E-07	BE047871.1	EST_HUMAN	z63406.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2281339 5'
7392	20071	33150	9.08	1.0E-07	N55081.1	EST_HUMAN	y43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7548	20218	33320	0.67	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7548	20218	33321	0.67	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7577	20246	33351	1.31	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7721	20385	33489	0.64	1.0E-07	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8114	20808	33941	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8114	20808	33942	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8853	21544	34691	2.78	1.0E-07	AA693576.1	EST_HUMAN	z151e10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:434348 3'
9170	21840	35005	0.97	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9617	22170	35353	0.46	1.0E-07	BE327843.1	EST_HUMAN	huz28406.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9838	22487	35689	2.77	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element;
9844	22495	35698	1.21	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
10382	23009		1.28	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12212	25188	30810	3.83	1.0E-07	BE048770.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12514	24884		1.87	1.0E-07	X5755.1	NT	h153c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:085722 085722
7181	19867	32840	0.84	9.0E-08	A1539382.1	EST_HUMAN	DJ1163J.1.1; Human lambda-Immunoglobulin constant region complex (germline)
9787	22438	35645	1.88	9.0E-08	AV734818.1	EST_HUMAN	h51b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080186 3'
11136	23804	37082	1.71	9.0E-08	A1891092.1	EST_HUMAN	AV734819 cda Homo sapiens cDNA clone cDABFB08 5'
11688	24283	37587	2.8	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
12168	24648		4.44	9.0E-08	A1251873.1	NT	OFR repetitive element;
583	15546		3.7	8.0E-08	A1811382.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1028	13788		0.72	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens partial steirin-1 gene
3532	16288		1.53	8.0E-08	BE795469.1	EST_HUMAN	wd18a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8638	21330	34474	3.05	8.0E-08	A1752367.1	EST_HUMAN	601580133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8638	21330	34475	3.05	8.0E-08	A1752367.1	EST_HUMAN	601580133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8627	22180	35364	2.93	8.0E-08	AW970883.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
10461	23107	36338	0.47	8.0E-08	AF111167.2	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11211	23874		2.1	8.0E-08	AF253417.1	NT	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
78	12904	25542	2.66	7.0E-08	Q02357	SWISSPROT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1340	14088	26784	13.91	7.0E-08	X04809.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
3563	16318	28965	1.15	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN) Rat mRNA for ribosomal protein L31
							DYNEIN HEAVY CHAIN (DYHC)

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3563	16318	28666	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10716	23405		1.67	7.0E-08	A153743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
11672	24267	37589	5.17	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12619	16318	28665	2.88	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12619	16318	28666	2.88	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12690	24975		1.88	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
788	13570	26230	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
798	13570	26231	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2363	15085	27824	2.97	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0168-191169-004-909 HT0168 Homo sapiens cDNA
3056	15824	28469	0.61	6.0E-08	7682473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4222	16963	26588	0.98	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7851	20546		0.69	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9227	21808		0.56	6.0E-08	AA827075.1	EST_HUMAN	ab56c05.s1 NCI_CGAP GC81 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ; RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11891	23967	37289	2.24	6.0E-08	P11369	SWISSPROT	Homo sapiens chromosome 21 segment HS21C009
11520	24120		1.33	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C103
83	12609	25547	3.72	5.0E-08	AL163303.2	NT	rh03b08.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element
2229	14957	27697	1.82	5.0E-08	AA488851.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
11914	24477		8.36	5.0E-08	P06681	SWISSPROT	QV0-C10225-131069-034-e12 C10226 Homo sapiens cDNA
12009	24599	31085	2.54	5.0E-08	AW851878.1	EST_HUMAN	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1754	14496	27185	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1754	14496	27196	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2888	15655		1.09	4.0E-08	AL078561.1	EST_HUMAN	DKFZp434J0428_t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0428 5'
3894	16844	28284	1.04	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6311	19082	32067	1.08	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8697	21389	34533	0.63	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9037	21727	34881	1.06	4.0E-08	L42571.1	NT	Cricetus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9545	22198		0.71	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10228	22876		0.68	4.0E-08	A1016342.1	EST_HUMAN	af78d12.s1 Soares_t04_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3'
10284	22932	36147	3.87	4.0E-08	A1050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MIER22 repetitive element ;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11009	23681	36839	1.71	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CAL-K-EXCHANGER ;
11009	23681	36840	1.71	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CAL-K-EXCHANGER ;
11031	23702	36889	4.02	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11031	23702	36970	4.02	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11919	25334		4.31	4.0E-08	W76159.1	EST_HUMAN	z165q03.r1 Soares_fetal_heart_Nbt-H19W Homo sapiens cDNA clone IMAGE:345558 5' similar to contains L1.1 L1 repetitive element ;
12549	24887		2.18	4.0E-08	AI343353.1	EST_HUMAN	tt656t1.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
5523	18321	31222	2.22	3.0E-08	BE018348.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z158 Q8Z158 SYNTAXIN 17 ;
6879	17855	30552	4.24	3.0E-08	A1792737.1	EST_HUMAN	qs76f11.y5 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
7439	20116	33205	1.66	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7649	20313		3.56	3.0E-08	AI496352.1	EST_HUMAN	tt63h09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q19537 Q19537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9798	22449		0.52	3.0E-08	AF055066.1	NT	Homo sapiens MHC class 1 region
10948	23628	35877	1.32	3.0E-08	AI218001.1	EST_HUMAN	qbt21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 3'
11566	24165	37477	61.58	3.0E-08	R86278.1	EST_HUMAN	yp12b10.s1 Soares_breast_3Nbt-HBst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT BINDING PROTEIN-1 (HUMAN);
11566	24165	37478	61.58	3.0E-08	R86278.1	EST_HUMAN	yp12b10.s1 Soares_breast_3Nbt-HBst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT BINDING PROTEIN-1 (HUMAN);
11888	24459		2.27	3.0E-08	R18420.1	EST_HUMAN	yg02f04.r1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element ;
201	13014		9.03	2.0E-08	AW302988.1	EST_HUMAN	xr87f08.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2767139 3'
221	13033		9.14	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Soares_total_fetus_Nbt2HF8_gw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element ; contains element MER15 repetitive element ;
484	13269	25805	1.01	2.0E-08	AF168349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
645	13424	26082	13.62	2.0E-08	AW886438.1	EST_HUMAN	MRO-O10080-240200-001-g08 OT0080 Homo sapiens cDNA
645	13424	26083	13.62	2.0E-08	AW886438.1	EST_HUMAN	MRO-O10080-240200-001-g08 OT0080 Homo sapiens cDNA
989	13735		24.4	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138863 6'
1320	14069	26743	2.38	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1734	14476		12.18	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845188 5'

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1847	14585		4.11	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2545	15280		1.71	2.0E-08	K00216.1	NT	Sheep His-rRNA-GUG
3202	15935	28618	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3202	15935	28619	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3840	16591		1.78	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161088-012-b03 ST0197 Homo sapiens cDNA
4373	17111		2.48	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
4903	17630		2.38	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Alu repetitive element;
5549	18346	31255	1.19	2.0E-08	AA813204.1	EST_HUMAN	aa80h11.s1 Soares testis NHT Homo sapiens cDNA clone 1377189 3'
5742	18534	31457	0.93	2.0E-08	AW088624.1	EST_HUMAN	xs32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3
7903	20598	33728	0.92	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element;
8009	20704	33932	1.35	2.0E-08	AA490121.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8983	21673		0.9	2.0E-08	AU139878.1	EST_HUMAN	eb02g06.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839874 3'
10416	23082	36281	0.79	2.0E-08	N78097.1	EST_HUMAN	AU139878 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10416	23082	36282	0.79	2.0E-08	N78097.1	EST_HUMAN	yw72022.l1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12184	24658		1.54	2.0E-08	AL163284.2	NT	yw72022.l1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
1499	15571	26931	1.16	1.0E-08	P31782	SWISSPROT	Homo sapiens chromosome 21 segment HS21C084
1768	14510	27211	1.45	1.0E-08	AF125348.1	NT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2044	14777		2.31	1.0E-08	BE141959.1	EST_HUMAN	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5512	18310	31211	4.85	1.0E-08	AJ010770.1	NT	PM2-HT0130-150989-001-f12 HT0130 Homo sapiens cDNA
7668	20332	33443	1.28	1.0E-08	P19474	SWISSPROT	Homo sapiens hyperton gene, exons 1-50
7834	20629	33756	0.52	1.0E-08	AL163302.2	NT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8028	20723	33855	0.64	1.0E-08	AF224659.1	NT	Homo sapiens chromosome 21 segment HS21C102
8028	20723	33856	0.64	1.0E-08	AF224659.1	NT	Homo sapiens chromodase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8445	21137	34275	1.94	1.0E-08	A015304.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9104	21792		0.45	1.0E-08	P09593	SWISSPROT	035a05.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9105	21793	34958	0.78	1.0E-08	BE072572.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
							PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9866	22516	35712	1.2	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10453	23089	36330	0.77	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11285	23948	37241	4.14	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12282	24715		2.82	1.0E-08	X31765.1	NT	Homo sapiens major histocompatibility locus class III region
4218	16959	29583	4.65	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4218	16959	29584	4.65	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9862	22610		0.52	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
6390	19159		0.62	8.0E-09	AL270615.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7164	19851	32820	7.66	8.0E-09	A183500.1	EST_HUMAN	qi86a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978984 3' similar to contains L1.13 L1 repetitive element;
7399	20594	33726	2.65	8.0E-09	AW900159.1	EST_HUMAN	qi42a07.x1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
8887	21678		2.65	8.0E-09	AA938892.1	EST_HUMAN	CM0-NN1004-100300-273-c06 NN1004 Homo sapiens cDNA qp74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1682575 3'
3593	16348		1.73	7.0E-09	D96842.1	NT	Homo sapiens DNA for 3-ketoad-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
7802	20487		0.61	7.0E-09	BF108755.1	EST_HUMAN	745a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;
7946	20841		0.82	7.0E-09	AA256200.1	EST_HUMAN	z60c05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element;
9159	21829	34993	2.91	7.0E-09	LC9709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10083	22731	35946	1.42	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10244	22892		0.5	7.0E-09	AA058626.1	EST_HUMAN	z58a07.s1 Soares retina N2b4-IR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element;
10571	23266		1.49	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2149	14879		0.89	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514.1_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434C0514 5'
4922	17650	30263	3.12	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-H05 HT0527 Homo sapiens cDNA
5296	18101	30760	11.59	6.0E-09	AW195764.1	EST_HUMAN	xn85h08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8475	21167	34311	0.93	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-H12 HT0446 Homo sapiens cDNA
8074	21763	34925	1.96	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10176	22824		3.76	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10632	23324	36561	1.44	6.0E-09	BF108755.1	EST_HUMAN	745a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11788	24388	37722	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMGS0003762 Human adult (K.Okuibo) Homo sapiens cDNA
1394	14141	26818	3.27	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-H10 HT0262 Homo sapiens cDNA
1845	14583	27298	1.06	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6316	19087	32071	1.73	5.0E-09	AA369454.1	EST_HUMAN	EST68748 Fetal lung II Homo sapiens cDNA 5' end
6748	17917	30581	0.76	5.0E-09	U68058.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8484	21176	34321	0.48	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
9895	22843	35855	2.22	5.0E-09	AW799687.1	EST_HUMAN	PM2-JM0053-240300-005-c09 UM0053 Homo sapiens cDNA
508	13282		2.12	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
944	13710		2.5	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1463	14200	26884	2.52	4.0E-09	Q558718	NT	Homo sapiens hypothetical protein (AF038168), mRNA
2016	14751	27478	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2016	14751	27480	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2430	16161	27885	6.07	4.0E-09	AA350878.1	EST_HUMAN	EST68385 Infant brain Homo sapiens cDNA 5' and similar to similar to heat shock protein, 80 kDa
7746	20442	33565	0.59	4.0E-09	AA405747.1	EST_HUMAN	zr04-c08.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8420	21113	34250	0.62	4.0E-09	T64942.1	EST_HUMAN	yf11a07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66804 3'
10779	23482	36704	2.06	4.0E-09	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
11011	23683	36943	1.47	4.0E-09	AI886401.1	EST_HUMAN	wm94H10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11061	23731		1.85	4.0E-09	AA185142.1	EST_HUMAN	zr34e12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:365278 5' similar to gb:U07807 DYNAMIN-1 (HUMAN);
2351	15073	27810	4.77	3.0E-09	BE222239.1	EST_HUMAN	hJ09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2557	15271	28008	1.2	3.0E-09	BE222239.1	EST_HUMAN	hJ09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2656	15396	28104	1.13	3.0E-09	P23249	SWISSPROT	MER18 repetitive element; PROTEIN MOV-10
3323	16088	28733	1.12	3.0E-09	BE222239.1	EST_HUMAN	hJ09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3371	16190		1.08	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element;
4076	16820		0.7	3.0E-09	X16674.1	NT	zr54a04.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4392	17129	29761	3.42	3.0E-09	AF175325.1	NT	Hi.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4476	17211	28636	1.65	3.0E-09	Q9Y3R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds 258.1 KDA PROTEIN C21ORF5 (KIA00933)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7800	20496	33617	1.19	3.0E-09	BE465780.1	EST_HUMAN	h80a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3184080 3' similar to TRC:O55081
10147	22785	36009	1.7	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN.;
10945	23824	36873	4.8	3.0E-09	BF108943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
10945	23824	36874	4.8	3.0E-09	BF108943.1	EST_HUMAN	772c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
794	13566		2.43	2.0E-09	X16674.1	NT	772c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1235	13984	26653	7.99	2.0E-09	AL163284.2	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1655	14401		7.48	2.0E-09	AL118573.1	EST_HUMAN	H. sapiens chromosome 21 segment HS21C084
2326	15051	27787	1.1	2.0E-09	Q873R5	SWISSPROT	DKFZp761B1710.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
3916	16668	28306	3.01	2.0E-09	O60241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
5076	17795	30411	0.85	2.0E-09	M23161.1	NT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5633	18428	31341	0.55	2.0E-09	A004082.1	EST_HUMAN	Human transposon-like element mRNA
6058	18638		0.57	2.0E-09	AL163249.2	NT	cd47b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6682	19589		0.83	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7351	20032	33110	8.4	2.0E-09	AA461430.1	EST_HUMAN	EST168142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7423	20100	33188	0.68	2.0E-09	W28834.1	EST_HUMAN	z63h06.11 Soares_tad_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains
7717	20381	33494	0.62	2.0E-09	AW862128.1	EST_HUMAN	Alu repetitive element;
8612	21304	34447	1.78	2.0E-09	AJ271735.1	NT	52d111 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11233	23896	37183	1.62	2.0E-09	AL163248.2	NT	MIR1-CT0352-240200-105-508 CT0352 Homo sapiens cDNA
12428	13566		22.07	2.0E-09	X16674.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12495	25403		2.41	2.0E-09	AA228070.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
12834	24934		1.75	2.0E-09	U82688.1	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
974	13739		0.72	1.0E-09	W78152.1	EST_HUMAN	nc11c02.11 NCI_CGAP_Py1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive
1087	13845	26503	2.01	1.0E-09	5031624	NT	element;
1087	13845	26504	2.01	1.0E-09	5031624	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
1630	14376		1.17	1.0E-09	AJ228041.1	NT	zdf79403.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to
2892	16559	28304	1.59	1.0E-09	U80017.1	NT	gbL02882 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
2926	16592	28336	3.25	1.0E-09	M28696.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2926	16592	28337	3.25	1.0E-09	M28696.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
3034	16800	28446	0.7	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	17478		6.4	1.0E-09	AA718297.1	EST_HUMAN	z185b03.s1 Soares_pitneal_gland_N3-IPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5418	18215	30923	0.66	1.0E-09	AL163283.2	NT	Alu repetitive element; contains element MER22 repetitive element;
5740	18532	31455	1.89	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6053	18833	31785	3.13	1.0E-09	P28694	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8289	20983	34124	0.85	1.0E-09	AL688474.1	EST_HUMAN	CIRCUMSPORZOITE PROTEIN PRECURSOR (CS)
10212	22860		2.92	1.0E-09	AL163283.2	NT	wc38b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
11789	24389		1.68	1.0E-09	AL163283.2	NT	MER25.11 MER25 repetitive element;
12333	25344	30717	2.25	1.0E-09	11418127	NT	Homo sapiens chromosome 21 segment HS21C083
12503	24857		1.35	1.0E-09	T83178.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1286	14036	28707	3.74	8.0E-10	AW867740.1	EST_HUMAN	ye24e05.r1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:118888 5'
							MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2836	15908	28256	4.41	8.0E-10	AB70071.1	EST_HUMAN	wc78t03.x1 Soares_Dieckgraebe_coton_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
6735	19589	32801	4.76	9.0E-10	AI452982.1	EST_HUMAN	SW_RL29_HUMAN P47914 603 RIBOSOMAL PROTEIN L29; contains element PTR5 repetitive element;
142	12957	25589	13.27	8.0E-10	U63630.2	NT	#48509.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
3337	16097	28748	0.88	8.0E-10	BE080748.1	EST_HUMAN	TR:O00372 O00372 PUTATIVE P150.;
4177	16917	28544	3.17	8.0E-10	AA376832.1	EST_HUMAN	Homo sapiens MCMA4 (MCMA4) and DNA-PKcs (PRKDC) genes, partial cds
9885	22515		2.44	8.0E-10	U36308.2	NT	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
685	13450	26107	9.36	7.0E-10	7706225	NT	EST88584 Small Intestine I Homo sapiens cDNA 5' and
685	13450	26108	9.36	7.0E-10	7706225	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
1618	14365	27055	2.24	7.0E-10	Q13342	SWISSPROT	Homo sapiens TPA inducible protein (LOC51588), mRNA
2013	14748		3.17	7.0E-10	P08548	SWISSPROT	Homo sapiens TPA inducible protein (LOC51588), mRNA
2584	15278		24.23	7.0E-10	P08547	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
3085	15850	28491	2.19	7.0E-10	X00856.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6092	18870	31836	4.18	7.0E-10	AA345220.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7316	19999	33078	1.08	7.0E-10	BF352883.1	EST_HUMAN	Hi sapiens DHFR gene, exon 3
7566	20228		1.48	7.0E-10	P36084	SWISSPROT	EST51247 Gall bladder II Homo sapiens cDNA 5' and
7875	20570	33888	1.6	7.0E-10	AF029701.2	NT	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7875	20570	33897	1.6	7.0E-10	AF029701.2	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
10209	22857	36073	1.67	7.0E-10	L08895.1	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
							Homo sapiens presenilin-1 gene, exons 1 and 2
							Homo sapiens MAD5/MEF2-family transcription factor (MEF2C) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
893	13602	26327	3.5	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf18 gene and C11orf17 gene
2684	15393	28132	1.21	6.0E-10	AJ424405.1	EST_HUMAN	h02d07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2065021 3'
4689	17423		2.7	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031089-012-g12 CT0254 Homo sapiens cDNA
8882	21374	34518	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2) (CD62E)
8882	21374	34519	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2) (CD62E)
9334	22187	36373	0.46	6.0E-10	P98073	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
11950	24503		2.16	6.0E-10	AW971823.1	EST_HUMAN	EST384012 MAG2 resequences, MAGL Homo sapiens cDNA
745	13518		7.27	5.0E-10	AL046804.1	EST_HUMAN	DKF7p434N219.1 434 (synonym: hess3) Homo sapiens cDNA clone DKF7p434N219 5'
3468	16224	28678	2.5	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
4931	17659	30269	1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7222	19907		1.51	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4042413 5'
9436	22114	35288	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9436	22114	35289	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
109	12630		1.17	4.0E-10	AJ221083.1	EST_HUMAN	qg08f09.x1 Soares melanocyte 2Nbl-IP8b9W Homo sapiens cDNA clone IMAGE:1756049 3' similar to contains LTR8.b2 LTR8 repetitive element;
567	13348	25976	0.74	4.0E-10	AA516260.1	EST_HUMAN	nf84e01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:324848 3'
1989	14725	27446	1.31	4.0E-10	AW594708.1	EST_HUMAN	hg58g03.x1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
2560	15294	28032	3.73	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7076	19767	32831	25.71	4.0E-10	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10095	22743	35957	0.49	4.0E-10	AW283243.1	EST_HUMAN	UIH-B12-ah1-a-07-Q-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10343	22890	36208	0.89	4.0E-10	AI287342.1	EST_HUMAN	ag83h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035663
895	13683	26329	3.65	3.0E-10	NS6113.1	EST_HUMAN	yj62f06.s1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:272863 3' similar to contains L1.1 L1 repetitive element;
1329	14078		4.72	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
4468	17234	29864	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4498	17234	29865	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5368	18169	30855	1.24	3.0E-10	N80109.1	EST_HUMAN	y21f08.s1 Soares multiple sclerosis 2NblHMSP Homo sapiens cDNA clone IMAGE:282782 3'
6110	18887	31858	2.52	3.0E-10	P20350	SWISSPROT	RHOMBLOID PROTEIN (VEINLET PROTEIN)
6258	19032	32007	3.43	3.0E-10	BE302870.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7660	20324	33432	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7660	20324	33433	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8629	21321	34463	1.2	3.0E-10	H87208.1	EST_HUMAN	ys74b12.e1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
8647	21638	34764	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
8647	21638	34765	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9240	21919		0.58	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10359	23008		2.37	3.0E-10	T65891.1	EST_HUMAN	yc11e12.L1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:80398 5'
10493	23139		1.34	3.0E-10	AA769284.1	EST_HUMAN	nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:128908 3'
12584	24907	31003	2.65	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
34	12862	25479	1.97	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
34	12862	25480	1.87	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1890	14627		1.96	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2085	15751		1.04	2.0E-10	BF875047.1	EST_HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5714	18507		2.54	2.0E-10	Q28640	SWISSPROT	(HPRG)
8156	18633	31800	1.37	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7279	18963	33039	6.47	2.0E-10	BE791082.1	EST_HUMAN	501588208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
7812	20807	33737	0.48	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7912	20807	33738	0.48	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9202	21871		0.99	2.0E-10	BF434596.1	EST_HUMAN	7c78d08.L1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3842303 3' similar to contains L1.13 L1 repetitive element;
11297	23988		1.37	2.0E-10	AI862153.1	EST_HUMAN	terf012.x1 Soares total fetus Nb21F8_9w Homo sapiens cDNA clone IMAGE:2043696 3'
1498	14245		1.87	1.0E-10	AW867767.1	EST_HUMAN	MFO-SN0038-290300-001-01 SN0038 Homo sapiens cDNA
1602	14348	27037	3.18	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXXA11 3'
2586	15300		3.16	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0226-197199-058-e08 CT0225 Homo sapiens cDNA
3491	16247	28901	0.89	1.0E-10	AW832812.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3528	16284		0.7	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3825	16284		1.03	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3896	16744		6.19	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4108	16851	29477	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4108	16851	29478	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4113	16858	29484	1.94	1.0E-10	AB031088.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4149	16891		1.84	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.51	1.0E-10	A1797745.1	EST_HUMAN	w62704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.L1 MER31 repetitive element;
6720	18035	32678	0.86	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7375	20055		0.85	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7583	20251	33357	0.55	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8138	20832	33968	1.04	1.0E-10	AW408930.1	EST_HUMAN	IB_9A4 Fetal brain library Homo sapiens cDNA
8553	21245		1.07	1.0E-10	AL288340.1	EST_HUMAN	qmr04e10.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.1 L1 repetitive element;
10102	22750		4.01	1.0E-10	AA081888.1	EST_HUMAN	zn23g08.l1 Strategene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
10831	23513	36754	2.65	1.0E-10	A038280.1	EST_HUMAN	cy85h03.x1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1672861 3'
11896	17913		1.71	1.0E-10	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
255	13063	25702	1.59	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-281089-018-c08 HT0203 Homo sapiens cDNA
2097	14828	27661	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
2097	14828	27682	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28796	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28796	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_j1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
4465	17201	29827	1.03	9.0E-11	AA775985.1	EST_HUMAN	ae7981.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5487	18286		3.83	9.0E-11	BE079780.1	EST_HUMAN	RC9-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10054	22702	36919	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST127872 Carabellum II Homo sapiens cDNA 5' and
10054	22702	36920	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST127872 Carabellum II Homo sapiens cDNA 5' end
12258	24703	31080	3.9	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506808 5'
3114	15879		8.33	8.0E-11	H18971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b8HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3945	16636	29334	0.7	8.0E-11	AI478617.1	EST_HUMAN	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161636 3'
4022	16768	29398	4.88	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
6674	16338		0.65	8.0E-11	AW166158.1	EST_HUMAN	x45h11.x1 NCI_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2621081 3' similar to contains MER10.11
1430	14177	26862	1.75	7.0E-11	AA330842.1	EST_HUMAN	MER10 repetitive element ;
3852	16602	29240	1.03	7.0E-11	AJ277548.2	NT	EST34392 Embryo, 6 week Homo sapiens cDNA 5' end
8396	21089	34224	2.05	7.0E-11	AF163864.1	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
10129	22777		1.17	7.0E-11	P11369	SWISSPROT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
403	13188	25837	7.01	6.0E-11	M55270.1	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
403	13188	25838	7.01	6.0E-11	M55270.1	NT	ENDONUCLEASE]
6822	16384	32398	0.67	6.0E-11	L44140.1	NT	Human matrix Gla protein (MGP) gene, complete cds
7593	20281	33369	3.65	6.0E-11	P08547	SWISSPROT	Human matrix Gla protein (MGP) gene, complete cds
8262	20956	34085	7.81	6.0E-11	AV727859.1	EST_HUMAN	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
9213	21892	36058	0.62	6.0E-11	BE063509.1	EST_HUMAN	(G6PD) gene, complete cds
11	12838	25451	1.48	5.0E-11	AL163283.2	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3359	12838	25451	1.9	5.0E-11	AL163283.2	NT	AV727859 HTC Homo sapiens cDNA clone HTCCSC08 5'
4203	16944	29571	1.36	5.0E-11	P49034	SWISSPROT	CM0-BT0281-031199-087-403 BT0281 Homo sapiens cDNA
6423	19191	32187	1.63	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C083
7430	20107	33194	14.05	5.0E-11	11415709	NT	Homo sapiens chromosome 21 segment HS21C083
1380	14127		1.94	4.0E-11	AA436042.1	EST_HUMAN	ALDEHYDE OXIDASE
2793	15498	28238	7.14	4.0E-11	BE885900.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2869	15735	28385	1.16	4.0E-11	AL163247.2	NT	Homo sapiens proteodherin beta 3 (PCDH3), mRNA
4576	17311	29939	0.85	4.0E-11	D44668.1	EST_HUMAN	zu01b12.f1 Soares testis NHT Homo sapiens cDNA clone IMAGE:730559 5'
5384	19153	32153	3.2	4.0E-11	P20095	SWISSPROT	601507531F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3909295 5'
5903	19841	32888	0.82	4.0E-11	AA442630.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
7274	18958		4.5	4.0E-11	AF224699.1	NT	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
9295	21962		1.79	4.0E-11	BE149425.1	EST_HUMAN	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
9562	22215	35402	0.9	4.0E-11	AI609753.1	EST_HUMAN	z45h10.f1 Soares testis NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR-G1055250
							G1055250 PHEROMONE RECEPTOR VN4. ;
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
							RC1-HT0256-210100-013-f08 HT0256 Homo sapiens cDNA
							tt82g12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:21056830 3' similar to WP-ZK353.1
							CE00385 ;

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12462	24930	31029	1.47	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1475	14222	26908	2.8	3.0E-11	6678077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NIM23B) (Nim2), mRNA
4243	16284		1.04	3.0E-11	AA308248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
940	13707	26372	1.97	2.0E-11	A1150502.1	EST_HUMAN	q38c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1162	13916	26580	3.99	2.0E-11	R24807.1	EST_HUMAN	yg43e12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1162	13916	26581	3.99	2.0E-11	R24807.1	EST_HUMAN	yg43e12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1608	14354	27042	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1608	14354	27043	4.86	2.0E-11	L17432.1	NT	COR3beta (COR3beta) genes, complete cds
1612	14359	27048	1.21	2.0E-11	A1126371.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
3191	15954	28607	7.58	2.0E-11	P10263	SWISSPROT	COR3beta (COR3beta) genes, complete cds
3320	16080	28730	1.11	2.0E-11	A478617.1	EST_HUMAN	qc51c10.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gp1.02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.1f L1 repetitive element;
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							tm54c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
3356	16116	28771	0.93	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
3488	16244		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4409	17146		0.68	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-s05 BT0316 Homo sapiens cDNA
4567	17302		0.72	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4882	17609		1.77	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-261089-014-s01 BT0258 Homo sapiens cDNA
6044	18824	31785	1.02	2.0E-11	AW877806.1	EST_HUMAN	QV2-PT0073-280300-108-108 PT0073 Homo sapiens cDNA
6218	18982	31968	1.87	2.0E-11	AA581028.1	EST_HUMAN	nc83105.1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7095	19784	32850	0.59	2.0E-11	BF592845.1	EST_HUMAN	P15898 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.;
7782	20477		0.56	2.0E-11	P37072	SWISSPROT	797c03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3442565 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
8123	21811		1.14	2.0E-11	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10184	22832	36046	5.44	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10413	23059	36277	1.12	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10413	23059	36278	1.12	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA

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11058	23726	36997	1.48	2.0E-11	AA035398.1	EST_HUMAN	ZK7g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11058	23728	36998	1.48	2.0E-11	AA035399.1	EST_HUMAN	ZK7g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11090	23760	37035	1.57	2.0E-11	AA281958.1	EST_HUMAN	Zs18b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685519 5'
12017	25332		1.64	2.0E-11	AA704195.1	EST_HUMAN	Z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12048	24567		3.54	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12073	24586	31123	1.87	2.0E-11	BF377898.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	D26217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12479	24840		3.14	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781	25035		3.37	2.0E-11	11417898	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
661	13437	26078	1.34	1.0E-11	AJ131018.1	NT	Homo sapiens SCL gene locus
1195	13947	26811	3.35	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1485	14232		2.36	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2030	14765	27494	1.13	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14953	27582	2.91	1.0E-11	AF000573.1	NT	Homo sapiens homogenitatis 1,2-dioxygenase gene, complete cds
3490	16246	28900	1.2	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-282-d12 BN0105 Homo sapiens cDNA
5249	18055	30683	16.83	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5741	18333	31458	0.63	1.0E-11	BF222846.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8101	20795	33928	3.15	1.0E-11	4885546	NT	MER10 repetitive element:
8480	21172	34317	5.44	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHIF2) mRNA
8946	21637	34782	1.89	1.0E-11	BF365119.1	EST_HUMAN	V73408.r1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:28186 5'
8946	21637	34783	1.89	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA
11267	23919	37212	1.62	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA
9697	22348	35542	1.07	9.0E-12	AL163300.2	NT	602164907F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
9697	22348	35543	1.07	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9237	21916		0.93	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
12125	24817		3.91	8.0E-12	AL271738.1	NT	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4613	17348	28982	1.16	7.0E-12	Q06904	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
11322	24013	37316	9.69	7.0E-12	AA704736.1	EST_HUMAN	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3535	16291		0.71	6.0E-12	AV730554.1	EST_HUMAN	Z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
4314	17053	29678	8.52	6.0E-12	AA732516.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF08 5'
6295	19068	32051	0.77	6.0E-12	AF020503.1	NT	mz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

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8894	21586	34723	1.04	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9374	21949		1.87	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER28.12
1020	13780	26442	3.62	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element;
3385	16144	28801	1.61	5.0E-12	BE047778.1	EST_HUMAN	EST04462 Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HFBDV33
3713	16468	29104	5.03	5.0E-12	AJ271736.1	NT	tz42b03.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281217 5'
5931	18715	31671	6.41	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5931	18715	31672	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6399	19168	32167	11.33	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6883	19424	32439	0.94	5.0E-12	AL040739.1	EST_HUMAN	EST388850 MAGe resequences, MAGN Homo sapiens cDNA
6842	19424	32439	1.16	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8126	20822	33959	1.33	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8566	21258		0.55	5.0E-12	AW887037.1	EST_HUMAN	z101g12.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
8893	21584		0.54	5.0E-12	AL079681.1	EST_HUMAN	RC1-OT0088-220300-011-b07 OT0088 Homo sapiens cDNA
9006	21688	34847	2.93	5.0E-12	AJ271735.1	NT	DKFZp434J0426.r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9323	21890	35181	0.88	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
10175	22823		4.45	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10262	22910	36120	0.78	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
10468	23114	36344	0.41	5.0E-12	6878754	NT	Homo sapiens chromosome 21 segment HS21C102
237	13047	25686	4.2	4.0E-12	AA700326.1	EST_HUMAN	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
238	13047	25686	4.03	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
4577	17312	28940	0.8	4.0E-12	AI889894.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
7619	20180		0.72	4.0E-12	BF445140.1	EST_HUMAN	bc28m05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
8141	20835		3.2	4.0E-12	AF109807.1	NT	had21b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.b2
8587	21278	34418	0.87	4.0E-12	AB042815.1	NT	MER7 repetitive element;
11019	23691	36854	4.2	4.0E-12	AJ228043.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
12375	24774		2.78	4.0E-12	U78027.1	NT	Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
602	13380	26011	4.27	3.0E-12	AW341883.1	EST_HUMAN	h113d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR:O14517 O14517 SMRP.;
602	13380	26012	4.27	3.0E-12	AW341883.1	EST_HUMAN	h113d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR:O14517 O14517 SMRP.;
5084	17803	30421	0.81	3.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
8365	18167	30853	1.52	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7854	20318		0.63	3.0E-12	AW854328.1	EST_HUMAN	RC3-CT0285-031089-011-h02 CT0255 Homo sapiens cDNA
8273	20887	34109	0.81	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPsin
9004	21694	34844	0.52	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPsin
10551	23247	38483	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10551	23247	38484	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1649	14385	27084	1.39	2.0E-12	AW802131.1	EST_HUMAN	IL6-UM0071-120400-085-a05 UM0071 Homo sapiens cDNA
4084	16836	29462	0.91	2.0E-12	J01684.1	NT	Rat U3A small nuclear RNA
4084	16836	29463	0.91	2.0E-12	J01684.1	NT	Rat U3A small nuclear RNA
4387	17124		2.03	2.0E-12	BE083506.1	EST_HUMAN	CNM0-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
4840	17570	30192	1.18	2.0E-12	O70308	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4840	17570	30193	1.18	2.0E-12	O70308	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
5189	17978	30491	0.77	2.0E-12	P11389	SWISSPROT	ENDONUCLEASE
6385	19154		2.8	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGE sequences, MAGL Homo sapiens cDNA
7075	19768	32830	3.74	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
7244	19928	33005	1.02	2.0E-12	BE173036.1	EST_HUMAN	MR0-HIT0559-200400-015-a08 HIT0559 Homo sapiens cDNA
7558	20228	33331	2.2	2.0E-12	11422229	NT	Homo sapiens Aa-like transposable element (ALTE), mRNA
9208	22087		1.84	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
9885	22635		11.12	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
			0.87	2.0E-12	AI334130.1	EST_HUMAN	qq0702.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.;
10412	23058	36276	0.87	2.0E-12	AI334130.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN.;
12032	24557		2.81	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12223	24680		2.5	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
			2.21	1.0E-12	AW627674.1	EST_HUMAN	h90a09.x1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element;
119	12838	25578	2.21	1.0E-12	AW627674.1	EST_HUMAN	h90a09.x1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element;
1980	14716		1.39	1.0E-12	AI871726.1	EST_HUMAN	wm5107.x1 NC1_CGAP_U02 Homo sapiens cDNA clone IMAGE:2438483 3' similar to contains L1.B3 L1 repetitive element;
3067	15833	28476	1.29	1.0E-12	AF000891.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3057	15633	28477	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3855	16005	28242	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3855	16005	28243	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5877	16663		2.25	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5850	18732		1.93	1.0E-12	Q8Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0981
6438	18206	32202	0.62	1.0E-12	AF226843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7016	19708	32784	2.07	1.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7050	19741	32802	11.32	1.0E-12	A1248533.1	EST_HUMAN	qh68a04.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7050	19741	32803	11.32	1.0E-12	A1248533.1	EST_HUMAN	qh68a04.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8606	21298	34442	1.16	1.0E-12	AA782323.1	EST_HUMAN	ec26d05.s1 Stratigene ovary (#837217) Homo sapiens cDNA clone IMAGE:2921317 3' similar to contains element
11273	23834		1.72	1.0E-12	AW468478.1	EST_HUMAN	LTR3 repetitive element;
11942	24497	37808	4.54	1.0E-12	AW962164.1	EST_HUMAN	EST374237 MAGG sequences, MAGG Homo sapiens cDNA
12150	24637		1.52	1.0E-12	A1738592.1	EST_HUMAN	w433h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
12294	25308		2.92	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
3618	16371		1	9.0E-13	AJ271795.1	NT	Homo sapiens Xq pseudautosomal region; segment 12
3927	16677	28320	0.96	9.0E-13	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9301	22154		2.67	9.0E-13	N89653.1	EST_HUMAN	za26b06.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3'
700	13475	26123	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	13475	26124	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1830	14569	27281	2.94	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8011	20706	33834	0.78	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8011	20706	33835	0.76	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10046	22894		3.08	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11779	24370	37701	1.67	8.0E-13	U68080.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S8A3N2T, TCRBV13S8A2T, TCRBV6S8P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P
7718	20382	33495	0.71	7.0E-13	A1884398.1	EST_HUMAN	wn31f09.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
7718	20382	33498	0.71	7.0E-13	A1884398.1	EST_HUMAN	wn31f09.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8133	20827		0.68	7.0E-13	Q85165	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12404	24788		3.05	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868813 5'
12617	24923		1.37	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
2094	14825	27558	6.75	6.0E-13	AL163207.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
3316	18076		0.74	5.0E-13	R78338.1	EST_HUMAN	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
3392	18151		1.54	5.0E-13	AA435773.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
5777	18521	32548	0.84	5.0E-13	P08083	SWISSPROT	y82f04.l1 Soares placenta Nb2fP Homo sapiens cDNA clone IMAGE:145769 5'
10767	23451	36883	2.72	5.0E-13	P07313	SWISSPROT	z77a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
1860	14598		2.23	4.0E-13	AW378014.1	EST_HUMAN	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
2462	15180		1.57	4.0E-13	AF003529.1	NT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
5409	18297	31195	5.51	4.0E-13	BE180131.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
7105	18783	32858	1.05	4.0E-13	AB037750.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
7512	20183	33277	0.94	4.0E-13	AA431528.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7620	20286		1.07	4.0E-13	N44281.1	EST_HUMAN	Homo sapiens mRNA for KIAA1328 protein, partial cds
8740	21432	34577	1.07	4.0E-13	AL043810.1	EST_HUMAN	G452763 COR1 MRNA ;
9402	22084	35235	0.45	4.0E-13	AA076907.1	EST_HUMAN	y933g05.l1 Soares melanocyte 2Nht-IM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR-A32895 A32895 t complex sterility protein - mouse ;
9819	22568	35764	4.94	4.0E-13	AI289831.1	EST_HUMAN	DKFZp434A0128_r1_434 (synonym: hbes3) Homo sapiens cDNA clone DKFZp434A0128 5'
11120	23789	37068	2.09	4.0E-13	AA435819.1	EST_HUMAN	7804H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7804H11
11120	23789	37067	2.09	4.0E-13	AA435819.1	EST_HUMAN	qn32a05.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Alu repetitive element
175	12887		4.94	3.0E-13	AF003528.1	NT	z778g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
845	13615		1.62	3.0E-13	AA430310.1	EST_HUMAN	z778g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							z768g08.l1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2370	15082	27831	1.26	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2483	15201		2.47	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2658	15378	28117	2.91	3.0E-13	BF372862.1	EST_HUMAN	CM3-FT0100-140700-242-H08 FT0100 Homo sapiens cDNA
3182	15945		2.97	3.0E-13	AA745844.1	EST_HUMAN	db18402 at NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
5452	18251	31140	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ;
5452	18251	31141	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ;
5902	18687	31635	0.62	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
							O75139 KIAA0844 PROTEIN. ;
7783	20478	33603	7.67	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7975	20670	33782	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
7975	20670	33783	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
10088	22748	35661	0.72	3.0E-13	AW695487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10575	23270		3.61	3.0E-13	AD54788.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10975	23651	36904	3.86	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-403 BT0281 Homo sapiens cDNA
11598	24187	37517	2.29	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
145	12660	25602	3.42	2.0E-13	U52111.2	NT	CDM protein (CDM), adrenoleukodystrophy protein >
282	13043	25663	2.06	2.0E-13	U23638.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1247	13096	26663	7.89	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3005	15771	28419	0.9	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3005	15771	28420	0.9	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3275	16036	28686	1.13	2.0E-13	BF431899.1	EST_HUMAN	hab7605.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3498	16254	28908	1.11	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4088	16831		1.34	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6032	18812	31772	4.7	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6113	18890		0.58	2.0E-13	X78417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6717	18632	32675	7.15	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
6854	19438	32451	0.65	2.0E-13	10835072	NT	Human sapiens N-myristoyltransferase 1 (NMT1), mRNA
6854	19438	32452	0.65	2.0E-13	10835072	NT	Human sapiens N-myristoyltransferase 1 (NMT1), mRNA
10355	23002	36219	3.87	2.0E-13	5031898	NT	Human sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12105	24602		3.48	2.0E-13	AW882155.1	EST_HUMAN	OMG-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
285	13091	25732	1.52	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
888	13637	26307	5.64	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1313	14081	26738	1.08	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2015	14750	27478	2.13	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_G080 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
4553	17288	28917	1.84	1.0E-13	BF340987.1	EST_HUMAN	THIR repetitive element
7810	20505	33628	0.78	1.0E-13	AA577812.1	EST_HUMAN	602038009F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4185868 5'
7810	20505	33627	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element
9990	22638		0.79	1.0E-13	O15481	SWISSPROT	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element
10189	22847	36063	0.53	1.0E-13	AF300701.1	NT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
11352	24042	37345	11.1	1.0E-13	BF108755.1	EST_HUMAN	Mus musculus osteofollicular protein tyrosine phosphatase mRNA, complete cds
11694	24462		2.26	1.0E-13	AV716377.1	EST_HUMAN	745e10.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28.b2 MER29 repetitive element
12563	24893		2.12	1.0E-13	AJ271735.1	NT	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 6'
324	13125	25761	1.81	9.0E-14	AA781159.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
325	13126	25762	3.05	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element
2504	15221		3.66	9.0E-14	AW861577.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element
2599	15313	28050	1.18	9.0E-14	AJ133127.1	NT	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2599	15313	28051	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2758	15463	28206	2.6	9.0E-14	AB038162.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
3109	15874	28513	3.96	9.0E-14	AW513298.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
							xx54f05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3'

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3232	13125	25761	0.84	9.0E-14	AA781158.1	EST_HUMAN	g24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3778	16530	29169	6.85	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4707	17439	30071	1.86	9.0E-14	AJ002163.1	NT	Seguinus oedipus gene for seminal vesicle secreted protein semenogelin I
3489	16245		1.27	8.0E-14	BE468263.1	EST_HUMAN	h271c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3637	16687		2.87	8.0E-14	R76269.1	EST_HUMAN	y72603.r1 Soares placentia NB2HP Homo sapiens cDNA clone IMAGE:144796 3'
9348	20419	33539	15.04	8.0E-14	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9460	22019	35180	3.69	8.0E-14	AA218316.1	EST_HUMAN	zq17c10.s1 Strategene fetal retina 637202 Homo sapiens cDNA clone IMAGE:629670 3'
11410	24059		1.72	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0268-261089-014-e01 BT0268 Homo sapiens cDNA
12302	24727	31056	2.46	8.0E-14	A1686118.1	EST_HUMAN	wc92h09.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326143 3'
1625	15574		4.77	7.0E-14	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
8818	21510		10.57	7.0E-14	AL163285.2	NT	MER10 repetitive element;
358	13156	25797	14.14	8.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
9722	22373	35572	2.6	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9722	22373	35573	2.6	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
604	13362	26014	5.46	6.0E-14	Q63120	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4693	17716	30322	1.41	5.0E-14	AW073791.1	EST_HUMAN	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5446	18245	31133	5.77	5.0E-14	P08547	SWISSPROT	x603b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1, L2 L1 repetitive element;
1101	15560		2.18	4.0E-14	P04928	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1870	14608	27319	5.9	4.0E-14	AJ007973.1	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
3735	18488		0.87	4.0E-14	AA046502.1	NT	Homo sapiens LGMD2B gene
4259	17000	29630	1.05	4.0E-14	N46328.1	EST_HUMAN	z687a03.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:487858 5'
7858	20553		0.59	4.0E-14	X87344.1	NT	y773c12.s1 Soares_multiple_sclerosis_ZN14MSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1, B L1 repetitive element;
12626	25414		7.02	4.0E-14	A1686224.1	EST_HUMAN	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, DOB, DQB2 and RING8, 9, 13 and 14 genes
930	13697	26361	1.88	3.0E-14	X95466.1	NT	wmt08c03.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element
							R. norvegicus mRNA for CPG2 protein

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4870	17597	30220	0.92	3.0E-14	AW265354.1	EST_HUMAN	xp_4512.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
4873	17600	30222	0.97	3.0E-14	7656864	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
6635	18397	32411	1.49	3.0E-14	A1420786.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
6635	18397	32412	1.49	3.0E-14	A1420786.1	EST_HUMAN	fa91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
6744	25099		0.62	3.0E-14	AL163248.2	NT	fa91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
8686	21378	34522	0.87	3.0E-14	N42105.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
10914	23594	36840	1.28	3.0E-14	BE888016.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
11201	17597	30220	7.19	3.0E-14	AW265354.1	EST_HUMAN	Y07b10.1 Soares melanocyte 2NHRM Homo sapiens cDNA clone IMAGE:270523 5'
12539	25282		1.68	3.0E-14	AL163285.2	NT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
381	13168	25811	3.71	2.0E-14	AJ271736.1	NT	xp_4512.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
381	13168	25812	3.71	2.0E-14	AJ271736.1	NT	Homo sapiens chromosome 21 segment HS21C085
674	15548	26091	9.05	2.0E-14	AL163303.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2387	16108		1.49	2.0E-14	AW372886.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
2467	15185		2.15	2.0E-14	7657528	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2528	15245	27863	1.19	2.0E-14	AL163209.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2542	15258		1.14	2.0E-14	BE222432.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2681	15390		0.95	2.0E-14	P08548	SWISSPROT	RC6-BT0377-091298-031-D12 BT0377 Homo sapiens cDNA
5437	18236	30950	0.8	2.0E-14	BF380661.1	EST_HUMAN	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
5533	18331	31236	0.92	2.0E-14	A812351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
5634	18429	31342	3.42	2.0E-14	U01317.1	NT	hw90g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element;
6784	19528		0.8	2.0E-14	BF380661.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6984	19577	32724	0.62	2.0E-14	4585709	NT	IL2-JT0072-240800-142-D07 UT0072 Homo sapiens cDNA
7185	19871	32945	1.25	2.0E-14	P56163	SWISSPROT	fa78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.L3 L1 repetitive element;
7407	20084	33167	22.12	2.0E-14	BE158761.1	EST_HUMAN	Human beta globin region on chromosome 11
7407	20084	33168	22.12	2.0E-14	BE158761.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
9817	22468	35671	0.57	2.0E-14	A1978795.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11) mRNA
10317	22564	36181	0.53	2.0E-14	A1741648.1	EST_HUMAN	ZINC-FINGER PROTEIN NEURO-D4
							IL2-HT0397-071298-024-D04 HT0397 Homo sapiens cDNA
							IL2-HT0397-071298-024-D04 HT0397 Homo sapiens cDNA
							hw59g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
							AV741648 CB Homo sapiens cDNA clone CBFBFBF04 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10679	23370	36812	4.88	2.0E-14	AW136800.1	EST_HUMAN	U1-H-B1-actw-a-10-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
11691	24180	37507	1.29	2.0E-14	AW083689.1	EST_HUMAN	xc36702.x1 NCL_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2586363 3' similar to contains MER1.13
12636	26284		2.28	2.0E-14	AF008191.1	NT	MER1 repetitive element ;
1045	13804	28463	1.88	1.0E-14	AL163246.2	NT	Homo sapiens putative G8 protein (GR6) gene, complete cds
1385	14132	26805	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C046
1385	14132	26808	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1994	14730	27452	12.44	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2182	14911	27843	4.55	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2409	15130	27868	3.56	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2945	15711	28363	1.79	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHIRP-II)
3165	15928	28576	5.42	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3166	15928	28577	5.42	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3668	16818	28255	1.97	1.0E-14	AA682894.1	EST_HUMAN	ee89c12.s1 Stragane schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4440	17178	28802	1.91	1.0E-14	AW275852.1	EST_HUMAN	xc39h10.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5719	18511	31432	2.42	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid-CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6576	25095	32351	11.5	1.0E-14	11437150	NT	Homo sapiens prolamin (mouse)-like 1 (PROML1), mRNA
6576	25095	32352	11.6	1.0E-14	11437150	NT	Homo sapiens prolamin (mouse)-like 1 (PROML1), mRNA
11818	15828	28576	3.05	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
11818	15828	28577	3.05	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
1570	14317	27002	2.06	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR), mRNA
2170	14899		1.43	9.0E-15	AF196779.1	NT	Homo sapiens transcription factor [GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α]
7395	20074	33152	4.51	9.0E-15	P21416	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7915	20610	33740	1.08	9.0E-15	BE903559.1	EST_HUMAN	601677750.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
12718	24691		2.36	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2814	13253		0.91	8.0E-15	BE261482.1	EST_HUMAN	601148632.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7081	19771	32836	1.14	7.0E-15	BF035327.1	EST_HUMAN	601456531.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662086 5'
10334	22981						xc77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element ;
973	13738	28403	8.64	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	18818	31549	1.02	6.0E-15	X73482.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
5829	18818	31550	1.02	6.0E-15	X73482.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
401	13186	25834	6.63	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2764	15469	28212	1.38	5.0E-15	U01328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbR1et gene, and sodium phosphate transporter (NPT3) gene, complete cds
3481	16217		1.03	5.0E-15	AW26817.1	EST_HUMAN	UHHBW0-qlb-g-10-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731219.3
10574	23259		2.4	5.0E-15	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE06.5
418	12829	25442	2.85	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6667	18332	32339	0.76	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
10694	20392	33505	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10694	20392	33506	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4192	18833		7.06	3.0E-15	N88432.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142.5 similar to ANF(CARDIODILATIN)
4872	17599		0.79	3.0E-15	P02485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
6716	19831		1.33	3.0E-15	Q84625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7179	19865	32937	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7179	19865	32938	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9825	22476		2.51	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351794.3 similar to contains MER19.11 MER19 repetitive element
10694	23385	36825	2.47	3.0E-15	AB026808.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12310	26315		1.81	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12814	26056		1.35	3.0E-15	AW877214.1	EST_HUMAN	GM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
243	13052	25692	3.6	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25798	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25798	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28910	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28911	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4049	16794	29423	1.08	2.0E-15	AW238499.1	EST_HUMAN	xp26101.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1 repetitive element;
4680	17315		2.46	2.0E-15	AI806335.1	EST_HUMAN	wf0706.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348923 3' similar to TR:Q61043 Q61043 NINEIN.;
6089	18887	31833	0.88	2.0E-15	BE562362.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6089	18887	31834	0.88	2.0E-15	BE562362.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7014	19708		1.5	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7171	19857	32928	2.82	2.0E-15	AA704195.1	EST_HUMAN	z377e03.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:480924 3'
7284	19977	33054	5.18	2.0E-15	W05084.1	EST_HUMAN	zaf7d10.r1 Scores_fetal_jung_NbHL10W Homo sapiens cDNA clone IMAGE:288675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE;
8804	21486	34642	2.88	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
8971	21681	34811	1	2.0E-15	AA397768.1	EST_HUMAN	z377g08.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
8971	21681	34812	1	2.0E-15	AA397768.1	EST_HUMAN	z377g08.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
8904	21971	35145	1.23	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201089-078-412 HT0244 Homo sapiens cDNA
8904	21971	35146	1.23	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201089-078-412 HT0244 Homo sapiens cDNA
10742	23428		5.66	2.0E-15	AJ271795.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12451	25338		2.04	2.0E-15	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12653	16256	28910	3.34	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12653	16256	28911	3.34	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2777	15482		2.39	1.0E-15	AI689884.1	EST_HUMAN	b26105.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
3011	15777	28427	1.35	1.0E-15	BE043584.1	EST_HUMAN	h440a02.y1 NCI_CGAP_Ox44 Homo sapiens cDNA clone IMAGE:2899162 5'
3139	15903	28548	1.28	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5138	17656		0.97	1.0E-15	AW021431.1	EST_HUMAN	d123a06.y1 Morton Fetal Cerebra Homo sapiens cDNA clone IMAGE:2484202 5'
6279	19052	32030	1.74	1.0E-15	T86763.1	EST_HUMAN	ye40e10.s1 Scores_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element;
6809	19647		2.12	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0568-270100-074-g05 BT0568 Homo sapiens cDNA
8131	20825	33961	0.86	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8319	21012	34149	4.56	1.0E-15	AI200876.1	EST_HUMAN	qf68h06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8319	21012	34150	4.56	1.0E-15	AI200876.1	EST_HUMAN	qf68h06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8937	21628	34770	0.67	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8940	21631	34774	1.78	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9148	21877	35042	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9632	22185	35370	0.94	1.0E-15	AA864653.1	EST_HUMAN	d137c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1
10720	23409	36651	3.8	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
12722	25148	36898	4.72	1.0E-15	AI783944.1	EST_HUMAN	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element
4469	17204	29830	0.98	9.0E-16	4503188	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
10915	23595	36841	2.04	9.0E-16	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone o-23105
11698	24291	37615	1.48	9.0E-16	AI244341.1	EST_HUMAN	q78a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
11698	24291	37616	1.48	9.0E-16	AI244341.1	EST_HUMAN	MER10 repetitive element
5615	16411	31324	0.71	7.0E-16	4885120	NT	q78a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
7241	19828	33001	1.49	7.0E-16	O88807	SWISSPROT	MER10 repetitive element
7241	19828	33002	1.49	7.0E-16	O88807	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
12675	25237		1.88	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2137	14867		8.38	8.0E-16	AW972611.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
1476	14223	26909	1.08	5.0E-16	AJ251154.1	NT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2687	16398	28134	2.17	5.0E-16	AJ992176.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
8954	22802	35808	0.54	5.0E-16	AL163248.2	NT	ye28c12.t1 Stratiene lung (#837210) Homo sapiens cDNA clone IMAGE:119082 5'
11504	24105	37418	3.6	5.0E-16	BF217368.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
12757	25018		14.19	5.0E-16	11418127	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2233	14981		1.81	4.0E-16	AB001523.1	NT	o60c04.s1 Soares_tetua_Nb21F8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element
2378	15100	27839	1.77	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
2378	15100	27840	1.77	4.0E-16	AW797168.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
3460	16208	28856	3.58	4.0E-16	Q16653	SWISSPROT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4121	16863	29489	5.02	4.0E-16	BE083875.1	EST_HUMAN	Homo sapiens gene for TMEIM1 and PWP2, complete and partial cds
4121	16863	29490	5.02	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
7612	20278	33396	46.82	4.0E-16	AL163284.2	NT	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
							QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
							MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
							PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C084

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8195	21865	35029	1.04	4.0E-16	11423181	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
11182	23847	37133	1.51	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
11851	24435	37778	1.44	4.0E-16	Q62832	SWISSPROT	FOLLISTATIN-RELATED PROTEIN PRECURSOR
12014	24547		2.04	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12109	24605	31087	2.51	4.0E-16	6812459	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
130	12845	25589	2.03	3.0E-16	AW022882.1	EST_HUMAN	dlf45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
130	12845	25590	2.03	3.0E-16	AW022882.1	EST_HUMAN	dlf45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
453	13239		1.5	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434P037 5'
463	13249		1.5	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1435	14182	28887	1.38	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2975	15741	28388	3.78	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3913	16663	29304	19.63	3.0E-16	T08169.1	EST_HUMAN	EST06060 Infant Brain, Benito Soares Homo sapiens cDNA clone HIBBA13 5' end
3939	16669		0.95	3.0E-16	U03887.1	NT	Human BXP-20 gene
5198	18004		0.99	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5529	18327	31230	1.79	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8558	21248	34987	4.26	3.0E-16	AI002836.1	EST_HUMAN	en98h05.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element ;
9780	22441		0.89	3.0E-16	BF690817.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4392032 5'
10019	22667	35883	5.57	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
951	13717		1.2	2.0E-16	AL163278.2	NT	Homo sapiens chromosoma 21 segment HS21C079
2385	15108		0.91	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2694	15403		1.06	2.0E-16	J03061.1	NT	Human SSANV-related endogenous retroviral LTR-like element
4157	16897	29526	1.16	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4447	17183	29807	0.98	2.0E-16	AI208733.1	EST_HUMAN	qg56103.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839187 3' similar to contains MER29.13
5104	17822	30439	0.79	2.0E-16	BE081178.1	EST_HUMAN	MER29 repetitive element ;
6842	19404	32419	0.89	2.0E-16	Q31125	SWISSPROT	RC3-BT0048-131189-003-H12 BT0048 Homo sapiens cDNA
7815	20281	33389	0.75	2.0E-16	AI470723.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
							ff16e11.x1 NCJ CGAP Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element ;
7967	20562	33689	2.14	2.0E-16	AI732837.1	EST_HUMAN	nz4706.x5 NCI_QCAP_P12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR-O54849 O54849
8058	20752	33883	0.57	2.0E-16	BE588026.1	EST_HUMAN	HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:008905 ;contains MER7.11 MER7 repetitive element ;
							782h09.x1 NCI_QCAP_P28 Homo sapiens cDNA clone IMAGE:3303521 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8038	20752	33884	0.57	2.0E-16	BE58028.1	EST_HUMAN	782109.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8425	21118	34256	0.81	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
8425	21118	34257	0.81	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
180	12592	25630	1.84	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
373	13198		29.66	1.0E-16	AA628582.1	EST_HUMAN	af39g11.x1 Soares fetal_Nb21F8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1903	14699	27414	2.37	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0149-070700-293-a10 BN0148 Homo sapiens cDNA
5635	18430	31343	0.75	1.0E-16	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6341	19111		27.85	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6479	19246	32246	3.39	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7453	19111		7.15	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9183	21853	33018	1.07	1.0E-16	AW875851.1	EST_HUMAN	QV2-PT0012-040400-124-c05 PT0012 Homo sapiens cDNA
3722	18475	29112	2.11	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6824	19388		2.2	9.0E-17	AI392984.1	EST_HUMAN	tg22e11.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element;
8007	20702		4.75	9.0E-17	AW150257.1	EST_HUMAN	x949g12.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element;
10124	22772		2.47	9.0E-17	AF200718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
897	13757		1.77	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3872	16622		0.87	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5496	25069	31183	3.7	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7175	19881		1.94	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1441	14188		3.44	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBc2), mRNA
6240	18046		3.3	7.0E-17	AF216660.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6588	18351	32365	8.05	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
198	13011	25653	8	8.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6221	18995	31971	1.64	6.0E-17	AW682772.1	EST_HUMAN	h81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978895 3' similar to contains L1.12 L1 repetitive element;
10190	22838	35053	0.46	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
412	12823	25436	2.97	5.0E-17	T64110.1	EST_HUMAN	yc05f08.f1 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
7486	20158	33250	2.09	5.0E-17	T81043.1	EST_HUMAN	y428b04.f1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:109327 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3626	16379	28020	0.69	4.0E-17	AA843697.1	EST_HUMAN	789605.61 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059528 3'
8282	22016	35184	1.07	4.0E-17	AW129165.1	EST_HUMAN	x220e04.x1 NCI_CGAP_K108 Homo sapiens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11475	24076	37388	2.64	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12027	24555		1.75	4.0E-17	AI073546.1	EST_HUMAN	045e04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR-Q16630
1477	14224		1.14	3.0E-17	D14547.1	NT	Human DNA, SINE repetitive element
2091	14822	27554	1.85	3.0E-17	AW119123.1	EST_HUMAN	xt89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3188	15961		1.18	3.0E-17	P36410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3633	16386	28026	1.94	3.0E-17	BE328522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
3633	16386	28027	1.94	3.0E-17	BE328522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
4970	17695		1.89	3.0E-17	BF511266.1	EST_HUMAN	UJH-B14-epg-c-06-Q-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
8166	20860	33992	5.16	3.0E-17	N68451.1	EST_HUMAN	zat14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.15 PTR5 repetitive element;
9601	22254	35439	6.58	3.0E-17	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10278	22927	36140	0.84	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10279	22927	36141	0.84	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
11994	24532		3.65	3.0E-17	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
12764	25023		1.44	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLC.DIF08 5'
343	13144	25782	3	2.0E-17	AI270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1858922 3' similar to contains Alu repetitive element;
344	13144	25782	2.17	2.0E-17	AI270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1858922 3' similar to contains Alu repetitive element;
967	13733		1.84	2.0E-17	AA722832.1	EST_HUMAN	zg81d04.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:399761 3'
2448	15167	27904	2.21	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2448	15167	27906	2.21	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2630	15636	28343	6.64	2.0E-17	P12038	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5282	18087	30745	1.88	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5282	18087	30746	1.88	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6171	18948		2.04	2.0E-17	AF055068.1	NT	Homo sapiens MHC class 1 region
6368	19167		1.16	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0810_1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0810 5'
7882	20677	33902	1.12	2.0E-17	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8366	21049	34188	1	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' and similar to glycogenin
9769	22420	35028	2.81	2.0E-17	BE288888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860815 5'
9804	22455	35657	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9804	22455	35668	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10159	22807	36025	4.82	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10278	22828	36138	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10278	22828	36139	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10307	22954	36169	0.49	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10307	22954	36170	0.49	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
733	19307	26164	3.68	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1703	14446		1.26	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1761	14503	27204	2.73	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2109	14940	27671	2.35	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2335	15059	27785	2.06	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	16309		1.3	1.0E-17	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4116	16958		7.37	1.0E-17	R09942.1	EST_HUMAN	Y30607.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
6368	19136		0.69	1.0E-17	AW468468.1	EST_HUMAN	he88e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.t1 LTR8 repetitive element;
6555	19320	32327	2.04	1.0E-17	A1185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6555	19320	32328	2.04	1.0E-17	A1185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6989	19682	32730	0.93	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8480	21182	34324	1.33	1.0E-17	BE062744.1	EST_HUMAN	QVQ-BT0269-101299-072-407 B10263 Homo sapiens cDNA
8907	22556	35751	0.88	1.0E-17	AW996538.1	EST_HUMAN	QV3-BN0046-220300-129-G10 BN0046 Homo sapiens cDNA
11394	24000	37304	2.09	1.0E-17	Q28624	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
11732	24325	37649	2.47	1.0E-17	AA453647.1	EST_HUMAN	z44805.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785489 3' similar to TR:G1263081
2474	15182	27832	0.95	8.0E-18	AA174078.1	EST_HUMAN	G1263081 MARINER TRANSPOSASE ;
6368	22060		3.31	8.0E-18	A1472167.1	EST_HUMAN	Zp18g712.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608682 3'
3763	16518	29153	1.52	8.0E-18		NT	q86d03.x1 Soares_NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
339	13140	25776	16.92	7.0E-18	AW316976.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA xx10p04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gclL20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
339	13140	25777	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7343	20024	33100	1.33	7.0E-18	AW867542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
12492	13140	25776	3.41	7.0E-18	AW316976.1	EST_HUMAN	RC3-OT0091-170300-011-403 OT0091 Homo sapiens cDNA
12492	13140	25777	3.41	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3289	18050	28688	1	6.0E-18	X71791.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN);
4696	17432		3.02	6.0E-18	P62181	SWISSPROT	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
8148	20842		2.84	6.0E-18	11428155	NT	RIBOSOMAL PROTEIN L4 (HUMAN);
8246	20840	34077	0.72	6.0E-18	AL163210.2	NT	Radii norvegicus partial Gdn/Prx-1 gene for glia-derived nectin/protease nectin 1, enhancer region
11078	23749	37024	1.61	6.0E-18	AL163246.2	NT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE)
11300	23660	37260	1.74	6.0E-18	X87344.1	NT	(TGASE C) (TGC)
12241	24692	31076	3.29	6.0E-18	U87928.1	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
1125	13881	28541	21.7	5.0E-18	AL280214.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
5047	17768	30384	0.98	6.0E-18	D61517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
5191	17899	30822	1.2	5.0E-18	AF087813.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
8620	21312	34454	6.25	5.0E-18	BE143312.1	EST_HUMAN	Human acortitate hydratase (ACO2) gene, exon 4
10899	23579	36828	3.47	5.0E-18	10242378	NT	qin05g11.x1 Soares_placenta_8to8weeks_2Nblp8to9W Homo sapiens cDNA clone IMAGE:1883668 3'
10899	23579	36829	3.47	5.0E-18	10242378	NT	similar to contains Alu repetitive element;
12398	24770		3.4	5.0E-18	AW867182.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#8635) Homo sapiens cDNA clone GEN-411F05
12695	24978		4.18	5.0E-18	AV650547.1	EST_HUMAN	5'
121	12939	25580	1.37	4.0E-18	BE044076.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
121	12939	25581	1.37	4.0E-18	BE044076.1	EST_HUMAN	MRO-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
1711	14454	27153	1.19	4.0E-18	AA621814.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
1892	14619		1.12	4.0E-18	AT738592.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
							MRI-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
							AV650547 GLC Homo sapiens cDNA clone GLCGA02 3'
							ho38h04.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28.b3
							MER29 repetitive element;
							ho38h04.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28.b3
							MER29 repetitive element;
							nc24f11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
							KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							wi33h08.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2188	14927	27682	1.33	4.0E-18	Q08430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,8-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
2198	14927	27683	1.33	4.0E-18	Q08430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,8-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
3772	16524	29162	0.68	4.0E-18	A1581586.1	EST_HUMAN	ar83b08.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5279	18084	30740	2.24	4.0E-18	A1017565.1	EST_HUMAN	cu23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5279	18084	30741	2.24	4.0E-18	A1017565.1	EST_HUMAN	cu23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
7745	20441		0.63	4.0E-18	AA746811.1	EST_HUMAN	rx64a08.s1 NCL_CGAP_A1M1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.12 L1 repetitive element;
10827	23607	36858	8.76	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
829	13599	28270	1.68	3.0E-18	AA814198.1	EST_HUMAN	cd23h11.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN P48782 40S RIBOSOMAL PROTEIN S5.;
909	13678	28340	3.47	3.0E-18	BE088634.1	EST_HUMAN	GM0-BT0690-210300-288-g07 BT0690 Homo sapiens cDNA
3931	16981	28322	1.47	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6730	18584	32599	5.64	3.0E-18	BE001071.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
10844	23528	36769	1.61	3.0E-18	BF218650.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
12497	24852		6.14	3.0E-18	AW022015.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
244	13053	28693	4.42	2.0E-18	AW836820.1	EST_HUMAN	QV1-LT0036-150200-070-g07 LT0036 Homo sapiens cDNA
1130	13886		62.93	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33565044 5'
5326	18129		3.19	2.0E-18	AA668810.1	EST_HUMAN	af63a07.s1 Soares_basils_NHT Homo sapiens cDNA clone IMAGE:1408832 3' similar to TR:O14577
5419	18218	30927	3.68	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A08 FROM TQ31, COMPLETE SEQUENCE.;
5419	18218	30928	3.68	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5788	18579		1.68	2.0E-18	BF347229.1	EST_HUMAN	60202184F1 NCL_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4156670 5'
6073	18852	31817	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
6073	18852	31818	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
6185	18962	31935	1.04	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
6226	19000	31977	5.18	2.0E-18	AW685853.1	EST_HUMAN	h94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978984 3' similar to contains MER19.12 MER19 repetitive element;
7336	20018	33096	0.81	2.0E-18	AA457919.1	EST_HUMAN	aa89d1.1.r1 StrataGene fetal refseq 837202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77;
8047	20741	33873	0.47	2.0E-18	BE436524.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA

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6947	22595	35798	1.66	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
6947	22595	35799	1.66	2.0E-18	AW151673.1	EST_HUMAN	MER10 repetitive element ; x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
10894	23574	36824	2	2.0E-18	AW470791.1	EST_HUMAN	MER10 repetitive element ; hs33d08.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2876488 3' similar to contains THR.b3
11796	24329	37653	3.91	2.0E-18	AW151289.1	EST_HUMAN	THR repetitive element ; xg47e09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
12174	13886		1.45	2.0E-18	BE256097.1	EST_HUMAN	MER8 repetitive element ; G01114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4382	17119		1.02	1.0E-18	T95406.1	EST_HUMAN	ye43g05.L1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains
5271	18077	30707	3.63	1.0E-18	AV653405.1	EST_HUMAN	L1 repetitive element ; AV653405 GLC Homo sapiens cDNA clone GLC0KE11 3'
5483	18282	31180	2.94	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5483	18282	31181	2.94	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6363	19133	32128	1.63	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8341	21034	34171	1.43	1.0E-18	AI146288.1	EST_HUMAN	cd89d08.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.11 L1 repetitive element ;
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRat gene, and sodium phosphate transporter (NPT3) gene, complete cds
9789	22450	35663	4.22	1.0E-18	U91328.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
12130	24621	31092	4.23	1.0E-18	AF003529.1	NT	z11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
532	13316	25952	5.34	9.0E-19	AA281981.1	EST_HUMAN	MER19 repetitive element ;
							z11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
533	13316	25952	3.24	9.0E-19	AA281981.1	EST_HUMAN	MER19 repetitive element ;
7747	20443		4.47	9.0E-19	F09688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23F05
8588	21280	34419	2.54	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8588	21280	34420	2.54	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11072	23742	37016	4.82	9.0E-19	AB032959.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
							z11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
11801	13316	25952	1.88	9.0E-19	AA281981.1	EST_HUMAN	MER19 repetitive element ;
1026	13786		1.25	8.0E-19	AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
4372	17110		1.04	8.0E-19	F09648	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8048	20742	33874	0.92	8.0E-19	BE158936.1	EST_HUMAN	MR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14970	27708	1.51	7.0E-19	4758139	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6384	19134	32129	2.34	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7109	16885	32359	0.9	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
9911	22560	35756	0.51	7.0E-19	A344951.1	EST_HUMAN	ib01c08.x1 NCI_CGAP_L128 Homo sapiens cDNA clone IMAGE:2052302 3'
12036	26397		2.05	7.0E-19	AA705684.1	EST_HUMAN	z60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436146 3'
3761	16513		1.34	6.0E-19	AW862930.1	EST_HUMAN	PMO-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA
4430	17166	29795	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4430	17166	29796	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4747	17479		1.3	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4897	17692	30301	1.04	6.0E-19	AL120817.1	EST_HUMAN	DKF7p762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKF7p762F192 5'
5767	18558	31485	5.36	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
10324	22971	36191	1.03	5.0E-19	AJ297689.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11525	24125	37431	7.45	5.0E-19	AW183726.1	EST_HUMAN	x97b02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element;
541	13324	26958	1.68	4.0E-19	AB007670.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2689	15398	28136	1.02	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
5311	18115	30773	0.97	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3633	16384	29219	1.04	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3633	16384	29220	1.04	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4253	16394	29622	0.99	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4253	16394	29623	0.99	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4413	17150	29777	1.12	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADG Homo sapiens cDNA clone ADCAMA11 5'
5198	18006		0.64	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7283	19988		2.79	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9359	20430	33548	1.15	3.0E-19	X89685.1	NT	MLmusculus mRNA for TPCK33 protein
12284	24709		23.34	3.0E-19	AF165820.1	NT	Homo sapiens photobin I protein (PBI) mRNA, complete cds
2565	16279	28017	21.33	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4411	17148		1.03	2.0E-19	AJ311783.1	EST_HUMAN	qs91a02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1015898 3' similar to TR-Q68388 Q68388 POL/ENV GENE:
5963	18745	31706	0.57	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'

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7238	18823	32988	0.93	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8228	20822	34061	8.08	2.0E-19	AA012854.1	EST_HUMAN	zsa34c08.t1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
9809	22460	35698	0.88	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
11828	24413	37760	1.33	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-404 BT0333 Homo sapiens cDNA
11828	24413	37751	1.33	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-404 BT0333 Homo sapiens cDNA
469	13255		1.87	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36383 10 5'
2161	14891	27628	1.58	1.0E-19	H30795.1	EST_HUMAN	y079g07.t1 Soares adult brain N2b4HB50Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
2723	15430		2.37	1.0E-19	D38044.1	NT	MER10 repetitive element;
2851	15819		4.95	1.0E-19	4758977	NT	Human gene for Ah-receptor, exon 7-9
3396	16154	28806	1.2	1.0E-19	AA634967.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
5983	18784	31728	2.38	1.0E-19	U12186.1	NT	ep48b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1383631 3' similar to contains MER37.12
6114	25419		0.83	1.0E-19	AA595527.1	EST_HUMAN	MER37 repetitive element;
7528	20189	33283	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
7628	20189	33284	0.86	1.0E-19	U08813.1	NT	repetitive element;
7895	25118		0.93	1.0E-19	AF200719.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
8349	21042	34178	1.75	1.0E-19	M64657.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
8840	21332		2.64	1.0E-19	T89920.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
9849	22301		0.46	1.0E-19	U60822.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
10087	22735	35960	23.03	1.0E-19	AW812259.1	EST_HUMAN	y072b02.t1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains
10087	22745	35960	1.46	1.0E-19	N44631.1	EST_HUMAN	OFR repetitive element;
11760	24351	37683	1.55	1.0E-19	U93163.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
6649	19314	32319	2.66	8.0E-20	7657286	NT	RC0-S10174-191098-031-505 ST0174 Homo sapiens cDNA
6649	19314	32320	2.66	8.0E-20	7657286	NT	y031e09.t1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:272872 5'
7418	20095	33180	1.34	8.0E-20	A1221371.1	EST_HUMAN	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1
7418	20095	33181	1.34	8.0E-20	A1221371.1	EST_HUMAN	(IMAGE-B1) genes, complete cds
3270	16031	28982	1.41	7.0E-20	BF328453.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6898	17972	30528	6.28	7.0E-20	AL138120.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8394	21087	34222	12.48	7.0E-20	AA557657.1	EST_HUMAN	qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
							qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
							PM4-AN0086-050900-003-a04 AN0086 Homo sapiens cDNA
							DKFZp547D092.t1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547D082 5'
							n48c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.b2
							MER29 repetitive element;

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8394	21087	34223	12.48	7.0E-20	AA557657.1	EST_HUMAN	n48c04.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.52
11714	24308		1.95	7.0E-20	6912633	NT	MER29 repetitive element;
3543	16298	28949	3.52	6.0E-20	P39188	SWISSPROT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4239	16980	28605	3.33	6.0E-20	BE622434.1	EST_HUMAN	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4556	17291		1.18	6.0E-20	AV725123.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
7015	19707	32763	1.07	5.0E-20	AF075301.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTO8TA01 5'
							AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
7846	20541	33688	5.28	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
							zh78d08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
7846	20541	33688	5.28	5.0E-20	W90525.1	EST_HUMAN	contains MER30.11 MER30 repetitive element;
8002	20897	33825	0.7	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8734	21428	34672	2.54	5.0E-20	AB028174.1	NT	Mus musculus MIMAN-g mRNA, complete cds
8734	21428	34573	2.54	5.0E-20	AB028174.1	NT	Mus musculus MIMAN-g mRNA, complete cds
8345	20416		0.94	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJB45024.1
1616	14363	27054	1.34	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5562	18359		0.8	4.0E-20	Q99880	SWISSPROT	HISTONE H2B C (H2B/C)
7826	20521		5.15	4.0E-20	AI874352.1	EST_HUMAN	t284g03.x1 NCI_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2283398 3'
10398	23042	36259	1.33	4.0E-20	AW937459.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2135	14885	27595	1.02	3.0E-20	U03888.1	NT	Human BXP21 gene
4185	16828	29557	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I14
							z436612.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
4582	17317	29944	1.05	3.0E-20	AA037816.1	EST_HUMAN	Human DNA, SINE repetitive element
8833	21525		2.85	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10219	22867	36078	0.63	3.0E-20	BF185284.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084943 5'
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
10501	23257		1.87	3.0E-20	P11369	SWISSPROT	ENDONUCLEASE
							q70c02.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1804803 3' similar to contains Alu repetitive element;
11496	24097	37408	1.5	3.0E-20	A1284244.1	EST_HUMAN	q70c02.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1804803 3' similar to contains Alu repetitive element;
11496	24097	37409	1.5	3.0E-20	A1284244.1	EST_HUMAN	q70c02.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1804803 3' similar to contains Alu repetitive element;
12051	24569	31118	2.65	3.0E-20	BE988422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
							x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW.FRS5_MOUSE
811	13582		3.12	2.0E-20	AW303888.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5.;

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1089	13847	26505	3.37	2.0E-20	AA516335.1	EST_HUMAN	nc89t09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224068
1089	13847	26506	3.37	2.0E-20	AA516335.1	EST_HUMAN	G1224068 ORF2: FUNCTION UNKNOWN. ;
2820	13582		2.38	2.0E-20	AW303888.1	EST_HUMAN	ng68t09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224068
4893	17620	30238	4.97	2.0E-20	Q28983	SWISSPROT	G1224068 ORF2: FUNCTION UNKNOWN. ;
4893	17620	30239	4.97	2.0E-20	Q28983	SWISSPROT	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW_RS5_MOUSE
5067	17788		5.98	2.0E-20	5174538	NT	P97481 40S RIBOSOMAL PROTEIN S6. ;
8017	20712	33843	0.81	2.0E-20	AA308457.1	EST_HUMAN	ZONADHESIN PRECURSOR
8089	21778	34942	8.6	2.0E-20	D10083.1	NT	ZONADHESIN PRECURSOR
8089	21778	34943	8.6	2.0E-20	D10083.1	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
12426	26141	30895	2.03	2.0E-20	H65371.1	EST_HUMAN	EST180328 Liver III Homo sapiens cDNA 5' end
12615	26057		1.39	2.0E-20	11437152	NT	Homo sapiens RGH1 gene, retrovirus-like element
2007	15525	27488	3.71	1.0E-20	AA281881.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
4406	17143	28772	1	1.0E-20	BF115158.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
6704	19538	32568	0.75	1.0E-20	AF049567.1	EST_HUMAN	Homo sapiens heparin-binding growth factor binding protein (HBP-17), mRNA
8061	21750	34908	2.04	1.0E-20	11418491	NT	z11d08.l1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
11541	24141	37450	2.62	1.0E-20	AF223391.1	NT	mer19 repetitive element ;
12171	24651		1.73	1.0E-20	AA420453.1	EST_HUMAN	hr94b08.l1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
2913	15679		0.98	8.0E-21	AJ003514.1	EST_HUMAN	repetitive element ;
11804	24468		2.62	8.0E-21	AW898189.1	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
8711	21403		2.15	8.0E-21	AW674891.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
11526	24126	37492	3.52	8.0E-21	AA808411.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12064	24579		4.49	8.0E-21	O21330	SWISSPROT	nc60g08.l1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1
2061	14793	27518	1.62	7.0E-21	P15900	SWISSPROT	repetitive element ;
2061	14793	27519	1.62	7.0E-21	P15900	SWISSPROT	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MIP12-8J21
3689	16442	29083	0.69	7.0E-21	AL163300.2	NT	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
4228	16969		5.58	7.0E-21	AA046502.1	EST_HUMAN	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW.NIAM_HUMAN
							O85169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
							cb71f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
							ATP SYNTHASE A CHAIN (PROTEIN 6)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							Homo sapiens chromosome 21 segment HS21C100
							z67a06.l1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'